

Access DB# 6350d

# SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

**If more than one search is submitted, please prioritize searches in order of need.**

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval  
 Reference Librarian  
 Biotechnology & Chemical Library  
 CM1 1E07 - 703-308-4498  
 jan.delaval@uspto.gov

## STAFF USE ONLY

Searcher: Jan  
 Searcher Phone #: 4498  
 Searcher Location: \_\_\_\_\_  
 Date Searcher Picked Up: 4/1/02  
 Date Completed: 4/1/02  
 Searcher Prep & Review Time: \_\_\_\_\_  
 Clerical Prep Time: 10  
 Online Time: 10

### Type of Search

NA Sequence (#) \_\_\_\_\_  
 AA Sequence (#) ☒ \_\_\_\_\_  
 Structure (#) \_\_\_\_\_  
 Bibliographic \_\_\_\_\_  
 Litigation \_\_\_\_\_  
 Fulltext \_\_\_\_\_  
 Patent Family \_\_\_\_\_  
 Other \_\_\_\_\_

### Vendors and cost where applicable

STN \_\_\_\_\_  
 Dialog \_\_\_\_\_  
 Questel/Orbit \_\_\_\_\_  
 Dr.Link \_\_\_\_\_  
 Lexis/Nexis \_\_\_\_\_  
 Sequence Systems ☒ \_\_\_\_\_  
 WWW/Internet \_\_\_\_\_  
 Other (specify) \_\_\_\_\_



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2002, 06:13:54 ; Search time 68.03 Seconds  
(without alignments)  
263.134 Million cell updates/sec

Title: US-08-162-407-6

Perfect score: 1242

Sequence: 1 MTVLAPAMSPPTLYLLLLLL.....RPGEQVPVPSPQDLLLVH 235

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR\_68:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	2 I38440	flt3 ligand - huma
2	864.5	69.6	245	2 S43293	FLT3/FLK2 ligand (
3	834	67.1	178	2 I39076	Flt3 ligand altern
4	768.5	61.9	231	2 A49265	FLT3/FLK-2 ligand
5	606.5	48.8	220	2 S43291	FLT3/FLK2 ligand (
6	606.5	48.8	220	2 I58343	flt3 ligand isofo
7	93	7.5	1217	2 T22672	hypothetical prote
8	92	7.4	661	1 TNBE12	74k alpha trans-in
9	89.5	7.2	474	2 I19543	hypothetical prote
10	89	7.2	387	2 I48201	adhalin - golden h
11	89	7.2	793	2 S60735	splicing factor SF
12	88.5	7.1	1386	2 T00257	hypothetical prote
13	88	7.1	753	2 J00532	OP protein - kenne
14	87.5	7.0	479	1 A32280	protein-tyrosine-p
15	87	7.0	910	2 A53137	tyrosine kinase re
16	86.5	6.9	590	2 A40437	glutamic acid-rich
17	86	6.9	299	2 T17832	hypothetical prote
18	86	6.9	485	2 A33647	sulfated surface g
19	86	6.9	746	2 T28004	hypothetical prote
20	85	6.8	366	2 A57374	Fc gamma (19c) rec
21	84	6.8	263	2 T03162	tegment protein 6
22	84	6.8	757	2 A39283	gamma-glutamyl car
23	83.5	6.7	199	2 E75630	hypothetical prote
24	83.5	6.7	530	2 A45690	transactivator EBN
25	83	6.7	1509	2 T19486	hypothetical prote
26	82.5	6.6	418	2 T19800	hypothetical prote
27	82.5	6.6	426	2 I36948	Ig epsilon-chain -
28	82.5	6.6	512	2 D40829	activin receptor 1
29	82.5	6.6	513	2 J01484	activin receptor p

30	82	6.6	106	2 T06479	proline/leucine-rl
31	82	6.6	854	2 T23837	hypothetical prote
32	81.5	6.6	485	2 C75460	hypothetical prote
33	81.5	6.6	488	2 S13423	stromelysin 3 (EC
34	81.5	6.6	958	2 T13593	hypothetical prote
35	81.5	6.6	1119	2 T50995	related to cytocke
36	81	6.5	196	2 B48232	cysteine-rich exte
37	81	6.5	209	2 A48232	cysteine-rich exte
38	81	6.5	388	2 S15591	probable transpos
39	81	6.5	428	1 EHHU	Ig epsilon chain C
40	80.5	6.5	636	2 J00047	class I cytol kinase
41	80.5	6.5	1176	2 T49482	hypothetical prote
42	80.5	6.5	1306	2 T13592	hypothetical prote
43	80.5	6.5	1402	2 T46707	translational initia
44	80	6.4	398	2 T52311	isopenicillin N ep
45	80	6.4	434	2 S74706	(S)-2-hydroxy-acid

## ALIGNMENTS

```
RESULT 1
I38440
flt3 ligand - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
C:Accession: I38440; I39075; S43292
R:Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe
Blood 83, 2795-2801, 1994
A:Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor fo
A:Reference number: I38440; MUID:94235842
A:Accession: I38440
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-235 <RES>
A:Cross-references: EMBL:U03858; NID:9494978; PIDN:AAA19825.1; PID:9494979
R:Lyman, S.D.; Stocking, K.; Davidson, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581
A:Accession: I39075
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-235 <RES>
A:Cross-references: EMBL:U29874; NID:91072036; PIDN:AAA90949.1; PID:91072037
R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zuckowski, S.; Bazan, J.F.;
Felt, A.; Menich, M.; Kelnier, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik
Nature 368, 643-648, 1994
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopo
A:Reference number: S43290; MUID:94195428
A:Accession: S43292
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-71, 'A', '73-235 <HAN>
A:Cross-references: GB:U04806; NID:9483844; PIDN:AAA17999.1; PID:9483845
A>Note: the authors translated the codon AGT for residue 25 as Met
C:Genetics:
A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3

Query Match 100.0%; Score 1242; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.8e-99;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTLYLLLLSSGSGTDCSPQHSPISSDPAVKIRELSDVLLQDYPTV 60
DB 1 MTVLAPAMSPPTLYLLLLSSGSGTDCSPQHSPISSDPAVKIRELSDVLLQDYPTV 60
QY 61 ASNLDDEELCGGLMKLVLAQRMERLKYAGSKMGLLERVNTETHPYTKCAFQPPSCL 120
DB 61 ASNLDDEELCGGLMKLVLAQRMERLKYAGSKMGLLERVNTETHPYTKCAFQPPSCL 120
QY 121 RRVQINIRSLQETSEQLVALKPWITRQNFRCLELQCGQPDSSTLRPPMSPRLATVPT 180
```

Db 121 RFVQTNISRLIQEISEQVIAVKPMTITQNSRCLCQCPDSSSLPPRPWSRPLAEAPPT 180

QY 181 APQPPLLLLLLPYGLLLAAAMCLHMQRTRRRPRRGEQVPVPSQDLLLLYEH 235

Db 181 APQPPLLLLLLPYGLLLAAAMCLHMQRTRRRRRRPRRGEQVPVPSQDLLLLYEH 235

RESULT 2  
S43293  
FLT3/FLK2 ligand (clone S109) - human  
C:Species: Homo sapiens (man)  
C:Date: 20-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-1999  
C:Accession: S43293  
R:Hannun, C.; Cuilpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kiehl, A.; Muench, M.; Kellner, G.; Namiikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A.  
Nature 368, 643-648, 1994  
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of hematopoietic  
A:Reference number: S43290; MUID:94195428  
A:Accession: S43293  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-245 <HMAN>  
A:Note: the authors translated the codon AGT for residue 25 as Met

Query Match	69.6%	Score	864.5	DB 2:	Length	245	
Best Local Similarity	73.0%	Pred.	No. 8.5e-67				
Matches	176	Conservative	7	Mismatches	27	Indels	31
						Gaps	3

  

QY	1	MTVLAPAMSPPTYYLLLLLLLLSSGLSGTODCSFQHSPISSDFPAVKIRELSDYLLQDPYTV	60
Db	1	MTVLAPAMSPPTYYLLLLLLLLSSGLSGMTGDCSFQHSPISSDFPAVKIRELSDYLLQDPYTV	60
QY	61	ASNLDEELCGMLRVLVAQRMWERLKTIVAGSKMGGLELRYVTEIHFVTKCAFQPPSCL	120
Db	61	ASNLDEELCGMLRVLVAQRMWERLKTIVAGSKMGGLELRYVTEIHFVTKCAFQPPSCL	120
QY	121	RFVQINISRLQETSEQVYALKPWITTRQNFSCLELEOCQPDSSITLPPWSPPLLENTAPT	180
Db	121	RFVQINISRLQETSEQVYALKPWITTRQNFSCLELEOCQPGA--PRQSPSPAACGALT	177
QY	181	APQF-----PLLLLLRLPVGLLLLAAMCCLHMORTRRRTTRPPGQVPPVPSF	227
Db	178	WPRPRPGEDTEAHNGESP-----ANGCLIAMQRIKLARGSLRPMWALIPSR	222
QY	228	Q 228	
Db	223	E 223	

```

RESULT      3      .
139076
Flt3 ligand alternatively spliced isoform - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: 139076
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S
Oncogene 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: 139075; MUID:96032581
A:Accession: 139076
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-178 <RES>
C:Cross-references: EMBL:U029874; NID:g1072036; PID:AAA90950.1; PID:g1072038
C:Genetics:
A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1

```

Query Match 67.1%; Score 834; DB 2; Length 178;  
Best Local Similarity 100.0%; Pred. No. 2,4e-64;  
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTVLAPAMSPPTYYLLELLLSGSGISGPODSPFHSPISSDFAKIRELSDYLLQDYPYV	60
Db	1	MTVLAPAMSPPTYYLLELLLSGSGISGPODSPFHSPISSDFAKIRELSDYLLQDYPYV	60
Qy	61	ASNLQDEELCGGLIRVLVLAQRMMERLKTVAQSGKQGLTERVMTIEHFVYKCAFQPPSCL	120
Db	61	ASNLQDEELCGGLIRVLVLAQRMMERLKTVAQSGKQGLTERVMTIEHFVYKCAFQPPSCL	120
Qy	121	RFVQTNISRLLEQTSQDLVALKPMWITRQNFNSRCLDQCP	160
Db	121	RFVQTNISRLLEQTSQDLVALKPMWITRQNFNSRCLDQCP	160

RESULT 4

A49265

fltk3/flk-2 ligand precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 08-Oct-1999

C:Accession: A49265; 149347; 149346; S43290

R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Holl

D.: Williams, D.E.; Beckmann, M.P.

Cell 75, 1157-1167, 1993

A:Title: Molecular cloning of a ligand for the fltk3/flk-2 tyrosine kinase receptor: a

A:Reference number: A49265; MUID:94084791

A:Accession: A49265

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-231 <LW>

A:Cross-references: GB:123636; NID:g439441; PIDN:AAA39436.1; PID:g439442

R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.

Oncogene 11, 1165-1172, 1995

A:Title: Structural analysis of human and murine fltk3 ligand genomic loci.

A:Reference number: 139075; MUID:96032581

A:Accession: 149347

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-163; 'G', 165, 'HYAG' <RES>

A:Cross-references: EMBL:U029875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041

A:Accession: 149346

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-197; 'L', 198-231 <RE2>

A:Cross-references: EMBL:U029875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040

R:Hamann, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.;

A.: Wnench, M.; Kelnar, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik

Nature 368, 643-648, 1994

A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic

A:Reference number: S43290; MUID:94195428

A:Accession: S43290

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-197; 'L', 198-231 <HAN>

A:Experimental source: clone T110

A:Note: the sequence from Fig. 2c is inconsistent with that from Fig. 2a in having 4-

C:Genetics:

A:Insertions: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3

C:Keywords: Transmembrane protein

Query	March	Similarity	61.9%	Score	768.5	DB	2	Length	231
	Best Local	Similarity	70.3%	Pred. No.	1.3e-58				
Matches	163	Conservative	17	Mismatches	43	Indels	9	Gaps	
Qy	1	MTVLAPAMSP--TTYLLLLLSGLSGTQDPSFQHSPISSDFAVKIRELSDYLQDPVT	59						
			:		:		:		:
Db	1	MTVLAPAMSPSSLLLLLSLSPCLRGTPDPCYFESHSPISNFKKRFELDLHLKQDPVT	60						
Qy	60	VASNLQDEELCGGLRLVLAQRMERLKTAVGASKQGLLEAVNTEIHFTVTKCAFPQPPSC	119						
			:		:		:		:
Db	61	VAVNLQDEKHCKALMSLPTLAQRWIEQLKTAVGSKMQLTLEDVNTETIHFTVSCFQPLREC	120						
Qy	120	LRFVQTNISRLQETSQDLVALKQWTR--QNSRCLTELQCPQDSSTLPPPMSERPLEAT	177						

Db 121 LRFQTNISHLKNQTCQGLLAKRCIOKACQNSRCLEVQCQDPSSLTLEPPRSIALTEAT 180

QY 178 APTAQPP - LLLLELLPVGSLLEAAAMCILHQWTRRRTERPGEQVPPVSP 227

Db 181 ELPPERRQQLLLLELLLPPLVLVLLAAMGLRMQRAARR ----GELHGVGLP 228

```

RESULT      5
S43291
FLR3/FLK2 ligand (clone T118) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S43291
R:Hannun, C.; Culpepper, J.; Campelli, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kie
felt, A.; Muench, M.; Kainer, G.; Nankawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A
Nature 368, 643-648, 1994
A:Title: Ligand for FLR3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic
A:Reference number: S43290; MUID:94195428
A:Accession: S43291
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-220 <HAN>

```

RESULT 6  
158343  
flt3 ligand isoform 5H - mouse  
C:Species: Mus sp. (mouse)  
C:Date: 26-Jul-1996 #sequence-revision 26-Jul-1996 #text-change 05-Nov-1999  
C:Accession: 158343  
R:Lyman, S.D.; James, L.; Escobar, S.; Downey, H.; de Vries, P.; Brasel, K.; Stocking, K.  
OncoGene 10, 149-157, 1995  
A:Title: Identification of soluble and membrane-bound isoforms of the murine flt3 ligand  
A:Reference number: 158343; MUID:95124710  
A:Accession: 158343  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-220 <RES>  
A:Cross-references: GB:S76459; NID:g913479; PIDN:AAB33069.1; PID:g913480

```

Query Match      48.8%; Score 606.5; DB 2; Length 220;
Best Local Similarity 61.5%; Pred. No. 9,4e-45;
Matches 13; Conservative 18; Mismatches 43; Indels 23; Gaps

QY 1 MTLVAPAMPSP-TTYVLLLLLLLSGLSTQOCSCFQHPSPSSDDFAVKIRELSDYLDQDPYV 59
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MTLVAPAMPSPNSLLLLLLLLLSPCLRTGTPDPCYFSHSPISSNPFKKFRELIDHLIKQDPYV 60
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 60 VASVLDDELGGIMRLVLAQRMRERKITYAGSGSMQGLLRVTNTEIHFYVKKCAQPPSPSC 119
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Db 61 VAVNIQDEKHCKALWLSLELAQRMTEQLKTVAWSKQTLLEDVNTETIHFNVSCTPQLPPEC 120  
QY 120 LRPQVNTSRLLQSEBGLVAKKPMTR--QNSRCLLEIQOPRSTLPPRWSRP---- 173  
Db 121 LRPQVNTSRLLKQTKCYDLLKPKCIGKACQNFRCLEVCQPSNG-----GPRQNHG 174  
QY 174 ---LEAPAPAPQPPLL-----LLLPVGLLLAA 201  
Db 175 ATRLLATALLVCPGLLPLVGTSHMFLPPLFSLFS 212

RESULT 7  
T22672  
hypothetical protein F54F12.1 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T22672  
R:Barlow, K.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: Z19597  
A:Accession: T22672  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1217 <MIL>  
A:Cross-references: EMBL:Z81548; NID:e1062020; PIDN:CB04464.1; GSPDB:GN00021; CESP:F54F12  
C:Genetics:  
A:Experimental source: clone F54F12  
A:Gene: CESP:F54F12.1  
A:Map position: 3  
A:Introns: 742/2; 826/1; 884/2; 922/3; 972/1; 1024/2; 1102/1

```

RESULT      8
TNBE12
74K alpha trans-inducing protein - human herpesvirus 3
C:Species: human herpesvirus 3, varicella-zoster virus
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999
C:Accession: C27342
R:Davidson, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1816, 1986
A:Title: The complete DNA sequence of varicella-zoster virus.
A:Reference number: A27345; MUID:86306657
A:Accession: C27342
A:Molecule type: DNA
A:Residues: 1-661 <DAV>
A:Cross-references: EMBL:X04370; NID:g59895; PIDN:CAA27895.1; PID:g60001
A:Genetics:
A:Gene: 12
A:Superfamily: herpesvirus 77K alpha trans-inducing protein
A:Keywords: trans-inducing protein; transcription regulation

```

Query Match	7.4%	Score	92	DB	1	Length	661
Best Local	Similarly	26.6%	Pred. No.	3.8			
Matches	61	Conservative	29	Mismatches	103	Indels	36
						Gaps	11

QY 19 LLSGSGSGTDCS----FQHSPISSDFAVKI--RELSDYLLQDYPTVYASNLQDEELCG-71  
 A:Accession: I48201  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-387 <RES>  
 A:Cross-references: EMBL:U21677; NID:g726481; PIDN:AAA81645.1; PID:g726482  
 C:Superfamily: mouse adhalin

Db 79 LTPSPVLQSTERSHSLGLHNNHNPESLVSCMSNDVHDCFMQRYMETIQCLDLKLISGD 138  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T19543

QY 72 GLWRVLVAQRMERLKVASCKMGLLERYN-----TEHFVTKCARQP---PPSCIRFV 123  
 A:Accession: T19543  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-474 <MTL>  
 A:Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2  
 A:Experimental source: Clone C28D4  
 A:Gene: CESP:C28D4.2  
 A:Map position: 4  
 A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Db 139 GLWVWYENTYMWOLKTYTGAEPVVTSEKYNKSKSTVLLFSSVYAKKPSRPFKSKI 197  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T19543

QY 124 OTNISRLQETSEQLVALKPWITRONFSRCLELQCPDSSTLPPMSP-RPLEATAPAP 182  
 A:Accession: T19543  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-474 <MTL>  
 A:Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2  
 A:Experimental source: Clone C28D4  
 A:Gene: CESP:C28D4.2  
 A:Map position: 4  
 A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Db 198 NSDYRGICQELREALGVQYKM---YEMR-----PDDPTNPSPDRIINQELAAVTAT 247  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T19543

QY 183 QPRLLLLLLPVGLLLAAAMCHMORTRRTPRPGEQVPPVSPDGL 231  
 A:Accession: T19543  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-474 <MTL>  
 A:Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2  
 A:Experimental source: Clone C28D4  
 A:Gene: CESP:C28D4.2  
 A:Map position: 4  
 A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Db 248 GYGMWMEFLDVID---ARVCRRLKLOFRIRIRGRASV---IPDDL 287  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T19543

## RESULT 9

hypothetical protein C28D4.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T19543

R:McMurray, A.

Submitted to the EMBL Data Library, November 1996

A:Reference number: Z19139

A:Accession: T19543

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-474 <MTL>

A:Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2

A:Experimental source: Clone C28D4

A:Gene: CESP:C28D4.2

A:Map position: 4

A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Query Match 7.2%; Score 89.5; DB 2; Length 474;  
 Best Local Similarity 24.1%; Pred. No. 4.2;

Matches 59; Conservative 29; Mismatches 82; Indels 75; Gaps 15;

QY 27 TQDC-----SFQHS-PISSDFAVKIREL-SYLLQDYPTVYASNLQDEELCGGLMRL 76  
 A:Accession: T19543  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-474 <MTL>  
 A:Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2  
 A:Experimental source: Clone C28D4  
 A:Gene: CESP:C28D4.2  
 A:Map position: 4  
 A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Db 65 TTCCVDLKKVSKRSDSAPISGELIFRARELCAYL-----GGAMRK 106  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: S60735; S60733

QY 77 VLAQRMERLKVASCKMGLLERYNTEHFVTKCARQPSCIR-FVQTNISRLQET- 134  
 A:Accession: S60735; S60733  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-474 <MTL>  
 A:Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2  
 A:Experimental source: Clone C28D4  
 A:Gene: CESP:C28D4.2  
 A:Map position: 4  
 A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Db 107 VKIEEF--RIRAITGG-MSNLLFLVELPAH-LTPIQMEPEKALLRVQCSDIDOLSESV 162  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: S60735; S60733

QY 135 -----SEQLVALKPWITRONFSRCLELQCPDSSTLPPMSPR-PLEATA 178  
 A:Accession: S60735; S60733  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-474 <MTL>  
 A:Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2  
 A:Experimental source: Clone C28D4  
 A:Gene: CESP:C28D4.2  
 A:Map position: 4  
 A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Db 163 VFTLLSERNLGPKMLGVPGRGFEQFIPSRALQCLEISKRGSLIAPIVARVHTLDAP 222  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: S60735; S60733

QY 179 PTPAPQPLLLLLPVGLLLAAAMCHMORTRRTP---RPGF-----QVPPVSPD 229  
 A:Accession: S60735; S60733  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-474 <MTL>  
 A:Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2  
 A:Experimental source: Clone C28D4  
 A:Gene: CESP:C28D4.2  
 A:Map position: 4  
 A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Db 223 PKBPQ-----TLQTAQWLERF---KKTAPAGERPIEMYLTOAKVPSDYEST 266  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: S60735; S60733

QY 230 LLVE 234  
 A:Accession: S60735; S60733  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-474 <MTL>  
 A:Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2  
 A:Experimental source: Clone C28D4  
 A:Gene: CESP:C28D4.2  
 A:Map position: 4  
 A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Db 267 ITVAQ 271  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: S60735; S60733

## RESULT 10

I48201

adhalin - golden hamster

C:Species: Mesocricetus auratus (golden hamster)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Jun-2000  
 C:Accession: I48201

R:Roberts, J. L.; Campbell, K. P.

FEBS Lett. 364, 245-249, 1995

A:Title: Adhalin mRNA and cDNA sequences are normal in the cardiomyopathic hamster.  
 A:Reference number: I48201; M0ID:95278335

A:Accession: I48201  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-387 <RES>  
 A:Cross-references: EMBL:U21677; NID:g726481; PIDN:AAA81645.1; PID:g726482  
 C:Superfamily: mouse adhalin

Query Match 7.2%; Score 89; DB 2; Length 387;  
 Best Local Similarity 23.4%; Pred. No. 3.7;

Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps 14;

QY 11 TTYLLLLLSGSGTDCSFGQHSPISSDFAVKIRELSYLLQDYPTVYASNLQDEELC 70  
 A:Accession: I48201  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-387 <RES>  
 A:Cross-references: EMBL:U21677; NID:g726481; PIDN:AAA81645.1; PID:g726482  
 C:Superfamily: mouse adhalin

Db 115 TTYRQRLILLI-----EDEGRPLPYQAEFLVRSYHVEVL---PSPANRFL--TAL 161  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: S60735; S60733

QY 71 GGLMRL-----VLAQRMERLKVASCKMGLLERYNTEHFVTKCARQPSCIR 110  
 A:Accession: S60735; S60733  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-474 <MTL>  
 A:Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2  
 A:Experimental source: Clone C28D4  
 A:Gene: CESP:C28D4.2  
 A:Map position: 4  
 A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Db 162 GGLMELELQDLNITSALDRGVRPLPIEGKKEGVYIKGSARPFSTCKMVASPDSYAR 221  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: S60735; S60733

QY 111 CARQPP--SC-----LRFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCPD 161  
 A:Accession: S60735; S60733  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-474 <MTL>  
 A:Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2  
 A:Experimental source: Clone C28D4  
 A:Gene: CESP:C28D4.2  
 A:Map position: 4  
 A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Db 222 CAGGQRPPLLSQYSLAHFVDMQNVSLVDKSVPEPLD-----EVPTPGD 266  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: S60735; S60733

QY 162 SSTLPPMSPRPLEAT-----APTAPQPLLLLLPVGLLLAAAMC----- 204  
 A:Accession: S60735; S60733  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-474 <MTL>  
 A:Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2  
 A:Experimental source: Clone C28D4  
 A:Gene: CESP:C28D4.2  
 A:Map position: 4  
 A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Db 267 GLEHDPFCPTPEATGCRPLADALVTLVPLVALLL---TLLVAYIMCRRREGQLKRD 323  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: S60735; S60733

QY 205 -----LHMQRTRRTPRP-----GROVPP-VSPQ-DLL 231  
 A:Accession: S60735; S60733  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-474 <MTL>  
 A:Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2  
 A:Experimental source: Clone C28D4  
 A:Gene: CESP:C28D4.2  
 A:Map position: 4  
 A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Db 324 MATSDIOMVHCHTTHGNTTEELROMAAREVPRPLSTLPMENVATGERLPPRVSAQVPL 383  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: S60735; S60733

QY 232 LEVH 235  
 A:Accession: S60735; S60733  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-474 <MTL>  
 A:Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2  
 A:Experimental source: Clone C28D4  
 A:Gene: CESP:C28D4.2  
 A:Map position: 4  
 A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Db 384 LDQH 387  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: S60735; S60733

## RESULT 11

splicing factor SF3a 120K chain - human

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: S60735; S60733

R:Kraemer, A.; Mulhauser, F.; Wersig, C.; Groening, K.; Bibe, G.

RNA 1, 260-272, 1995

A:Title: Mammalian splicing factor SF3a120 represents a new member of the SUPR family

A:Reference number: S60733; M0ID:96079958

A:Accession: S60735

A:Status: nucleic acid sequence not shown

A:Molecule type: protein

A:Residues: 1-793 <KRA>

A:Cross-references: EMBL:X85237; NID:g899297; PIDN:CAA59494.1; PID:g899298

A:Accession: S60733

A:Molecule type: protein

A:Residues: 51-62; 82-94; 270-275; 397-414; 448-463 <KRA2>

A:Gene: GDB:SF3A120; PRP21; SAP114

A:Cross-references: GDB:9955873

A:Map position: 22q12.1-22qter

C:Superfamily: human splicing factor SF3a 120K chain; ubiquitin homology

C:Keywords: pre-mRNA splicing

F:714-790/Domain: ubiquitin homology <UBH>

Query Match 7.2%; Score 89; DB 1; Length 793;  
 Best Local Similarity 22.3%; Pred. No. 8.4;

Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

QY 4 LAPAWSPTTYLLLLLSGSGTDCSFGQHSPISSDFAVKIRELSYLLQDYPTVYASN 63  
 A:Accession: I48201  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-387 <RES>  
 A:Cross-references: EMBL:U21677; NID:g726481; PIDN:AAA81645.1; PID:g726482  
 C:Superfamily: mouse adhalin

Db 401 LPPAPAPDEVLY-----SPITGE--KI-----PASK 424  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: S60735; S60733

QY 64 LDQBELCGGLMRLVLAQRMERLKVASCKMGLLERYNTEHFVTKCARQPSCIR 107  
 A:Accession: S60735; S60733  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-474 <MTL>  
 A:Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2  
 A:Experimental source: Clone C28D4  
 A:Gene: CESP:C28D4.2  
 A:Map position: 4  
 A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

```

Db 425 MOENHRIG-----LLDPRLMEQBRDSIREKQSDDEVYAPAGLIDIESLKLQALR-RTDIFG 478
QY 108 VTKCA-----FQPPPSCLRF-----VQTNISRLQETSEQLVALKPMI 145
Db 479 VEETAIKGIKEEETIOKREEKVTWDGSGSMARQQAQANIT--LQROIATIKHAKGLV 536
QY 146 -----TRONF--SRCLELOCOP-----DSSTLP-----PMSPRPLEAT-----APT 180
Db 537 PEDTKKEIGSKRENEITQQPPPPSSATNIFSSAPITSVRRPPMPPTVTYVSAVPV 596
QY 181 APORPLLLLLLPGVLLLAAMCLHMORTR-----RRTPRPGEOYPP--VPSP 227
Db 597 MRRPMSVVALRPGOSVIALMPRTIHARINVPMPSPAPRIMARPPMTVPTAFVAP 656

```

## RESULT 12

```

T00257
hypothetical protein KIAA0476 - human
C:Species: Homo sapiens (man)
C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C:Accession: T00257
R:SeKI, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
DNA Res. 4, 345-349, 1997
A:Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human
A:Reference number: 214085; MUID:98116662
A:Accession: T00257
A>Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1386 <SEK>
A:Cross-references: EMBL:AB007945; NID:g3413913; PIDN:BAA32321.1; PID:g3413914
A:Experimental source: brain
C:Genetics:
A:Note: KIAA0476

```

```

Query Match 7.1%; Score 88.5; DB 2; Length 1386;
Best Local Similarity 23.1%; Pred. No. 17;
Matches 53; Conservative 28; Mismatches 85; Indels 63; Gaps 12;

```

```

QY 21 SSGLSGTODCSFOHSPISDFRAVKIRELSYLLDYPYTVASNLQDELC---GGLMKL 76
Db 1104 SAGASGSKDAPVGGP-----GPLYSDRRCLLA--LDEPOLCNGHMGASRR 1148
QY 77 VLAQRMRLKTVAGSKMOGLLERVTEIHFTKCAFQPPSCLEFQVTNISRLOETSE 136
Db 1149 VESGMAVLSPLVLRKELESIVENEGSEV-----LALPELSANPITFMNLMYQRL-- 1201
QY 137 QLVALKPMTIRQNSRCLLEOCO--PDSSTLPPPW--SPRPLEA-----TAPTAQPP 185
Db 1202 RLPSILPELVLAS-----CDGSHSQAPSPMLTPDPASVQVRLMDVLTDPDNSCP 1253
QY 186 LLLLLLLEFVGLLLAAMCLHMORTRRTPRPGEOVPPVPSEQDILLVE 234
Db 1254 LYLVL-----WRVHSQ--IPQRYVWPG-----VVPASLSTALLE 1284

```

## RESULT 13

```

J00532
Op protein - Kennedy yellow mosaic virus
C:Species: Kennedy yellow mosaic virus
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999
C:Accession: J00532
R:Ding, S.; Keese, P.; Gibbs, A.
J. Gen. Virol. 71, 925-931, 1990
A:Title: The nucleotide sequence of the genomic RNA of Kennedy yellow mosaic tymovirus-
A:Reference number: J00532; MUID:90218040
A:Accession: J00532
A:Molecule type: mRNA
A:Residues: 1-753 <DIN>
A:Cross-references: GB:D00637; NID:g221969; PIDN:BAA00531.1; PID:d1000986; PID:g221970
A:Experimental source: Strain Jervis Bay isolate

```

```

Query Match 7.1%; Score 88; DB 2; Length 753;
Best Local Similarity 22.3%; Pred. No. 9.6;
Matches 41; Conservative 19; Mismatches 58; Indels 66; Gaps 7;

```

```

QY 100 RVNTEIHFTVCAEQPPPSCLRF-----VQTNIS-----RLQETSEQLVALKPMITR 147
Db 420 RLSTQPPSSPQTSSPPRRPRTDASGIQTLASPPSKRKESLPRSHQ-----PRSHK 475
QY 148 QNFSR-----CLELQCPDSSSTLPPWSPRPLEATVTAQRPRLLLLLLP----- 193
Db 476 RNLRRHSALRLPLRPHRTKTPQHPAVPQ--TAGPRTNRPPTKKIRLHPKSGERNHSP 533
QY 194 -----VGLLLLAAMCLHMORTRRTPRPGEOYPPVPS 226
Db 534 PPDVHDCQPSPTSHVYGYRRLLGSGISLPEKLAFW-----RRKSPNPARHLLPPPP 586
QY 227 PQDL 230
Db 587 PRKL 590

```

## RESULT 14

```

A32290
protein-tyrosine-phosphatase (EC 3.1.3.48) cdc25 homolog string - fruit fly (Drosophila)
C:Species: Drosophila melanogaster
C>Date: 05-Oct-1989 #sequence_revision 25-Apr-1997 #text_change 11-Jun-1999
C:Accession: A32290; S12008
R:Edgar, B.A.; O'Farrell, P.H.
Cell 57, 177-187, 1989
A:Title: Genetic control of cell division patterns in the Drosophila embryo.
A:Reference number: A32290; MUID:89195217
A:Accession: A32290
A:Molecule type: mRNA
A:Residues: 1-479 <EDG>
A:Cross-references: GB:M24909; NID:g158507; PIDN:AAA28916.1; PID:g158508
R:Jimenez, J.; Alphey, L.; Nurse, P.; Glover, D.M.
EMBO J. 9, 3565-3571, 1990
A:Title: Complementation of fission yeast cdc2(+) and cdc25(+) mutants identifies c
A:Reference number: S12008; MUID:91006056
A:Accession: S12008
A:Molecule type: mRNA
A:Residues: 1-227, 'A', 229-479 <JIM>
A:Cross-references: EMBL:X57495; NID:g7706; PIDN:CAA40732.1; PID:g7707
A:Gene: Flybase:stg
A:Cross-references: Flybase:FBgn0003525
A:Function:
A:Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine
A:Pathway: Initiation of mitosis
A:Note: cdc25 activates the cdc2 protein kinase by dephosphorylating it
C:Superfamily: protein-tyrosine-phosphatase string; cdc25-type protein-tyrosine-phosp
C:Keywords: cell cycle control; mitosis; phosphoprotein; phosphoric monoester hydroly
F:252-456/Domain: cdc25-type protein-tyrosine-phosphatase homolog <PR>
F:379/Active site: Cys (phosphocysteine intermediate) #status predicted
F:385/Binding site: substrate phosphate (Arg) #status predicted

```

```

Query Match 7.0%; Score 87.5; DB 1; Length 479;
Best Local Similarity 22.9%; Pred. No. 6.3;
Matches 56; Conservative 34; Mismatches 76; Indels 79; Gaps 14;

```

```

QY 1 MIVLAPAMSPPTIYLL-----LLLSGLSGTQCSFOHSPISDFRAVKIRELSYLLDQVP 57
Db 72 MGLLSPEGSPQRFQIVROPKILPANGVSS-----DHTPARS-FRI-ENSLSS-----T 117
QY 58 VIVASNLQDEELCGGLMRLVLAQRMRLKTVAGSKMOGLLERVTEIHFTVTKCAFOPP 117
Db 118 CSMESMSDE-----YMLFEMESQSO-----QTALGF-----P 146
QY 118 SCLRFVQTNISRLQETSEQLVALKP--WTRQNFSCRLEL--QCQPDSSSTLPPWSPRP 173
Db 147 SGLN-----SLISQIKIQEAPAKSPAGLSMRPSVRRCLSMTESNTSTTTPPKTPE- 199

```





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2002, 06:16:39 ; Search time 68.97 Seconds

(without alignments)  
124.927 Million cell updates/sec

Title: US-08-162-407-6

Perfect score: 1242

Sequence: 1 MVLAPAWSPFTYLLLL...RPGEOVPPVSPDLLVEH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 3664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	1 FLJ3L_HUMAN	P49771 homo sapien
2	768	61.8	232	1 FLJ3L_MOUSE	P49772 mus musculu
3	92	7.4	661	1 ARI2_VZVD	P09264 varicella-z
4	89.5	7.2	941	1 GBR2_HUMAN	O75899 homo sapien
5	89	7.2	387	1 SGCA_MESAV	O64255 mesocricetu
6	89	7.2	793	1 S3A1_HUMAN	O15459 mus musculu
7	87.5	7.0	415	1 TNRG_MOUSE	P50284 mus musculu
8	87.5	7.0	479	1 MPIP_DROME	P20483 drosophila
9	87	7.0	910	1 DDRL_RAT	O63474 rattus norv
10	87	7.0	911	1 DDRL_MOUSE	O03146 mus musculu
11	86.5	7.0	1394	1 CNG4_BOVIN	O28181 bos taurus
12	86	6.9	485	1 SSGP_VOLCA	P21997 volvox cart
13	85	6.8	282	1 ATRF5_HUMAN	O972d1 homo sapien
14	85	6.8	366	1 FCGN_RAT	P13399 rattus norv
15	84	6.8	582	1 MNT_HUMAN	O09583 homo sapien
16	84	6.8	732	1 YF48_HUMAN	O9hcm4 homo sapien
17	83.5	6.7	671	1 Z282_HUMAN	O9udv7 homo sapien
18	83	6.7	758	1 VKGC_HUMAN	P38435 homo sapien
19	81.5	6.6	488	1 MML1_HUMAN	P24447 homo sapien
20	81.5	6.6	591	1 MNT_MOUSE	O08789 mus musculu
21	81.5	6.6	2124	1 Y192_HUMAN	O93074 homo sapien
22	81	6.5	283	1 ATRF5_MOUSE	O70191 mus musculu
23	81	6.5	387	1 SGCA_MOUSE	P82350 mus musculu
24	81	6.5	428	1 EPC_HUMAN	P01854 homo sapien
25	81	6.5	1248	1 DIAL_HUMAN	O06010 homo sapien
26	80.5	6.5	1402	1 IFAG_RABIT	P41110 oryctolagus
27	80	6.4	397	1 CEFPL_STRCL	P18549 streptomyce
28	80	6.4	940	1 GBR2_RAT	O08871 rattus norv
29	80	6.4	1174	1 KPCI_COCH	O42632 cochliobolu
30	80	6.4	1794	1 YAV1_SCHPO	O10172 schizosacch
31	79	6.4	805	1 TGM6_YEAST	P53086 saccharomyc
32	78.5	6.3	251	1 HXB4_HUMAN	P17483 homo sapien
33	78.5	6.3	382	1 AVRB_RAT	P38445 rattus norv

## ALIGNMENTS

```

RESULT 1
ID FLJ3L_HUMAN STANDARD: PRT: 235 AA.
AC P49771:
DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, last sequence update)
DT 20-AUG-2001 (rel. 40, last annotation update)
DE SL CYTOKINE PRECURSOR (FMS-RELATED TYROSINE KINASE 3 LIGAND) (FLT3
DE LIGAND).
GN FLT3LG
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94195428; PubMed=8145851;
RA Hannum C., Cuipepper J., Campbell D., McClanahan T., Zurawski S.,
RA Bazan J.F., Kastelein R., Hudak S., Wagner J., Matsen J., Luh J.,
RA Duda G., Martina N., Peterson D., Menon S., Shanafelt A.,
RA Muench M., Rosner G., Namikawa R., Rennick D., Roncarolo M.G.,
RA Zlotnik A., Rosner O., Dubreuil P., Birbaumer D., Lee F.;
RA "Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of
RT haematopoietic stem cells and is encoded by variant RNAs.";
RT Nature 368:643-648(1994).
RL [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94235842; PubMed=8180375;
RA Lyman S.D., James L., Johnson L., Brasel K., de Vries P.,
RA Escobar S.S., Downey H., Spielt R.R., Beckmann M.P., McKenna H.J.;
RT "Cloning of the human homologue of the murine flt3 ligand: a growth
RT factor for early hematopoietic progenitor cells.";
RL Blood 83:2795-2801(1994).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=96032581; PubMed=7366977;
RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
RA Escobar S.;
RT "Structural analysis of human and murine flt3 ligand genomic loci.";
RL Oncogene 11:1165-1172(1995).
CC - FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
CC FACTORS AND INTERLEUKINS.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. A SOLUBLE FORM
CC IS ALSO PRODUCED BY ALTERNATIVE SPLICING.
CC - ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
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CC -----

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RT \*Identification of a GABAB receptor subunit, gb2, required for functional GABAB receptor activity.\*  
 RL J. Biol. Chem. 274:7607-7610(1999).  
 RN [8]  
 RP R1A-R2 INTERACTION.  
 RX MEDLINE=2023752; PubMed=10773016;  
 RA Sullivan R., Chateauent A., Coulombe N., Kolakowski L.F. Jr.,  
 RA Johnson M.P., Hebert T.E., Ethier N., Bellef M., Metters K.,  
 RA Abramovitz M., O'Neill G.P., Ng G.Y.K.;  
 RT "Coexpression of full-length gamma-aminobutyric acid(B) (GABA(B)) receptors with truncated receptors and metabotropic glutamate receptor 4 supports the GABA(B) heterodimer as the functional receptor.";  
 RL J. Pharmacol. Exp. Ther. 293:460-467(2000).  
 CC -1- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G-PROTEINS THAT INHIBITS ADENYL CYCLASE ACTIVITY, STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS, INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND ANTIHYPOTENSION.  
 CC -1- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO HAPPEN.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A PERQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE PLASMA MEMBRANE.  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 2A (SHOWN HERE), 2B AND 2C; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALA AND MEDULLA. WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.  
 CC -1- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.  
 CC -1- STIMULATORY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS. GABA-B RECEPTOR SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AJ012188; CAA09942.1; -  
 DR EMBL: AF056085; AAC63228.1; -  
 DR EMBL: AF057123; AAC63383.1; -  
 DR EMBL: AF095724; AAC63384.1; -  
 DR EMBL: AF095784; AAC30389.1; -  
 DR EMBL: AF074483; AAD03336.1; -  
 DR EMBL: AF069755; AAC99345.1; -  
 DR EMBL: AF099033; AAD45867.1; -  
 DR InterPro: IPR001828; ANF\_Receptor.  
 DR InterPro: IPR000337; GPCR\_Mgr.  
 DR Pfam: PF00003; 7tm\_3; 1.  
 DR Pfam: PF01094; ANF\_receptor; 1.  
 DR PRINTS: PR00248; GPCRMR.  
 DR PRINTS: PR01176; GABABRECEPTR.  
 DR PRINTS: PR01177; GABAB1RECEPTR.  
 DR PRINTS: PR01178; GABAB2RECEPTR.  
 DR PROSITE: PS00999; PRO\_RICH; 1.  
 DR PROSITE: PS00979; G\_PROTEIN\_RECCEP\_F3\_1; FALSE\_NEG.

DR PROSITE: PS00980; G\_PROTEIN\_RECCEP\_F3\_2; FALSE\_NEG.  
 DR PROSITE: PS00981; G\_PROTEIN\_RECCEP\_F3\_3; FALSE\_NEG.  
 DR PROSITE: PS00982; G\_PROTEIN\_RECCEP\_F3\_4; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KW postsynaptic membrane; Colled coll; Alternative splicing;  
 KW Polymorphism.  
 KM SIGNAL 1 41  
 FT CHAIN 42 941  
 FT  
 FT DOMAIN 42 483  
 FT TRANSMEM 484 504  
 FT DOMAIN 505 522  
 FT TRANSMEM 523 543  
 FT DOMAIN 544 551  
 FT TRANSMEM 552 572  
 FT DOMAIN 573 597  
 FT TRANSMEM 598 618  
 FT DOMAIN 619 654  
 FT TRANSMEM 655 675  
 FT DOMAIN 676 691  
 FT TRANSMEM 692 712  
 FT DOMAIN 713 720  
 FT TRANSMEM 721 741  
 FT DOMAIN 742 941  
 FT DOMAIN 781 819  
 FT CARBOHYD 90 90  
 FT CARBOHYD 298 298  
 FT CARBOHYD 389 389  
 FT CARBOHYD 404 404  
 FT CARBOHYD 453 453  
 FT VARSPLIC 902 927  
 FT VARSPLIC 929 941  
 FT  
 FT VARIANT 628 628  
 FT  
 FT VARIANT 869 869  
 FT  
 FT CONFLICT 6 6  
 FT CONFLICT 12 12  
 FT CONFLICT 424 424  
 SQ SEQUENCE 941 AA; 105821 MW; 09F173DB0673C5D CRC64;  
 Query Match 7.28; Score 89.5; DB 1; Length 941;  
 Best Local Similarity 44.18; Pred. No. 5.1;  
 Matches 26; Conservative 2; Mismatches 22; Indels 9; Gaps 3;  
 QY 170 SPRPLEATAPAPPP-----LLLLLLPVGLLLAAACMLHWRTRRTPRGQVPPV 224  
 DB 3 SPRSGGPPPPPPPPPPPPPARLLLLLLPLPLPLAAGW--GW---AKGAPRPPSSPPL 56  
 RESULT 5  
 SCGA\_MESAU STANDARD; PRT; 387 AA.  
 AC Q64255;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE ALPHA-SARCOGLYCIN PRECURSOR (ALPHA-SG) (ADHALLIN) (50 KDA DYSTROPHIN-DE ASSOCIATED GLYCOPROTEIN) (50DAG).  
 GN SCGA.  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI-Taxid=10036;  
 OX [1]  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SYRIAN; TISSUE=Heart muscle;  
 RX MEDLINE=98054328; PubMed=9391120;  
 RA Sakamoto A., Ono K., Abe M., Jasmin G., Eki T., Murakami Y.,  
 RA Masaki T., Itoyo-Oka T., Hanaoka F.;

RT "Both hypertrophic and dilated cardiomyopathies are caused by mutation of the same gene, delta-sarcoglycan, in hamster: an animal model of RT disrupted dystrophin-associated glycoprotein complex." RT Proc. Natl. Acad. Sci. U.S.A. 94:13873-13878(1997).

RA [2] SEQUENCE FROM N.A.

RC STRAIN-FIB: TISSUE-Skeletal muscle;

RX MEDLINE=95278335; PubMed=7558576;

RA Roberds S.L., Campbell K.P.: "Adhalin mRNA and cDNA sequence are normal in the cardiomyopathic hamster.";

RL FBS Lett. 364:245-249(1995).

CC -1- FUNCTION: COMPONENT OF THE SARCOGLYCAN COMPLEX, A SUBCOMPLEX OF THE DYSTROPHIN-GLYCOPROTEIN COMPLEX WHICH FORMS A LINK BETWEEN THE F-ACTIN CYTOSKELETON AND THE EXTRACELLULAR MATRIX.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, SARCOLEMMAL (POTENTIAL).

CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SKELETAL AND HEART MUSCLE.

CC -1- SIMILARITY: BELONGS TO THE SARCOGLYCAN ALPHA/EPSILON FAMILY.

CC -----

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CC EMBL: D83651; BAA12025.1; -

DR EMBL: U21677; AAA81645.1; -

DR Cytoskeleton; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 23

FT CHAIN 24 387

FT DOMAIN 24 290

FT TRANSMEM 291 311

FT DOMAIN 312 387

FT DOMAIN 209 335

FT CARBOHYD 174 174

FT CARBOHYD 246 246

FT SEQUENCE 387 AA; 43326 MW; D8599C0FAF646C3F CRC64;

Query Match 7.2%; Score 89; DB 1; Length 387; Best Local Similarity 23.4%; Pred. No. 2; Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps 14;

QY 11 TTYVLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPYVANSNLODEELC 70

DB 115 TTRQRLLLI-----EDPEGRLPYQAEFLVRSNDEVL---PSTANRFL--TAL 161

QY 71 GGLMRL-----VLQRMKMERLKYAGSKMOGLLEVNTEHFVT-----K 110

DB 162 GGLMELDELQLLNTLSALDRGRVRLPIEGKKEGVYIKVGSATPFSCCLKWVSPDSYAR 221

QY 111 CAEPQPP--SC-----LRFVQTNISRLQETSEQLVAKPWITRONFSRCLEOCOPD 161

DB 222 CAQGQPRLLSCYDLSLAFHFRDMQCNVSLVKSVPEDL-----EYPIPGD 266

QY 162 SSTLPWPSPRPLEAT-----APTAPQRPRLLLLLPVLGLLLAAMC----- 204

DB 267 GILHDFPFCPTREATGRDELADALVTLVPLVALLL---TLLAYIMCRRREGQLKRD 323

QY 205 -----LHMQRTRRRTRPR-----GEQVPP--VPSPQ--DLL 231

DB 324 MATSDIOMVHHCTIHGNTIELROMAARREVPRLSTLPMFNVTGERLPPRVDSAYPLI 383

QY 232 LVFH 235

DB 384 LDQH 387

RESULT 6

S3A1 HUMAN

ID S3A1 HUMAN STANDARD; PRT; 793 AA.

AC 015459; 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE SPLICING FACTOR 3 SUBUNIT 1 (SPLICOSOME ASSOCIATED PROTEIN 114) (SAP DE 114) (SFA120).

GN SFA1 OR SAP114.

GN Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96079598; PubMed=7489498;

RA Kremer A., Mulhauser F., Wersig C., Groning K., Bilbe G.;

RT "Mammalian splicing factor Sfa120 represents a new member of the SURF family of proteins and is homologous to the essential splicing factor PRP21p of Saccharomyces cerevisiae.";

RL RNA 1:260-272(1995).

RN [2]

RP SEQUENCE FROM N.A.

RA Bentley D., Blandford M.;

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

RP [3]

RP CHARACTERIZATION OF THE SPLICOSOME.

RX PubMed=10882114;

RA Das R., Zhou Z., Reed R.;

RT "Functional association of U2 snRNP with the ATP-independent M1. Cell 5:779-787(2000).

CC -1- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SFA3 REQUIRED FOR 'A' COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT BINDING OF SFA3/SFB COMPLEX UPSTREAM OF THE BRANCH SITE IS ESSENTIAL, IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.

CC -1- SUBUNIT: COMPONENT OF SPLICING FACTOR SFA3 WHICH IS COMPOSED OF THREE SUBUNITS: SFA3A/SAP61, SFA3A2/SAP62, SFA3A1/SAP114. SFA3A ASSOCIATES WITH THE SPLICING FACTOR SFB3 AND A 12S RNA UNIT TO FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP).

CC INTERACTS WITH SFA3.

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

CC -1- TISSUE SPECIFICITY: UBQUITIN-LIKE EXPRESSED.

CC -1- SIMILARITY: CONTAINS 1 UBQUITIN-LIKE DOMAIN.

CC -1- SIMILARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRP21.

CC -----

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CC EMBL: X85237; CA59494.1; -

DR EMBL: AC004997; AAC23435.1; -

DR MIM: 605595; -

DR InterPro: IPR000061; SURF.

DR InterPro: IPR000626; Ubiquitin.

DR Pfam: PF001805; Surp; 2.

DR Pfam: PF00240; ubiquitin; 1.

DR SMART: SM00213; UBO; 1.

DR PROSITE: PS50053; UBQUITIN\_2; 1.

KW SPLICOSOME; mRNA processing; mRNA splicing; Nuclear protein; Repeat.

FT REPEAT 52 94

FT REPEAT 166 208

FT DOMAIN 707 793

FT DOMAIN 10 16

FT DOMAIN 118 122

FT DOMAIN 260 267

FT DOMAIN 369 372

POLY-PRO.

POLY-GLN.

POLY-GLU.

POLY-PRO.

FT DOMAIN 557 560 POLY-PRO.  
 FT DOMAIN 672 675 POLY-PRO.  
 SO SEQUENCE 793 AA: 88886 MW: 725961EC4577305C CRC64;

Query Match 7.28; Score 89; DB 1; Length 793;  
 Best Local Similarity 22.3%; Pred. No. 4.6;  
 Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

QY 4 LAPAMSPPTVLLLLLSGLSGTQDSFQHSPISSDFAVKIRELSYLLQDYVTVASN 63  
 DB 401 LPPAPADELV-----SPITGE---KI-----PASK 424  
 QY 64 LODELGGIMRLVLAQRME-RLKTV-----AGSKQGLLERYNTEIHF 107  
 DB 425 MOEHMRIG-----LIDPRWIEQQRDSIREKQSDDEVAYAPGLDIESLKLQALR-RTIDFG 478  
 QY 108 VTKCA-----FQPPSPCLNF-----VQTNISRLQETSOLVALKPMI 145  
 DB 479 VESTATIGKKIGEERIOKPEEKVTWDGHSQMARQQAQANIT--LOEOIEAIHKAGLV 536  
 QY 146 -----TRONF--SRCLAQCCP-----DSSFLP-----PWSRPLEAT---APT 180  
 DB 537 PEDDTKKTGKIPKPNELPQQPPPPSSATNIPSSAPITTSVPRPTMPPEVATTYVSAVPV 596  
 QY 181 APOPPLLLLLPYGLLLLAAMCLHMQRTR-----RRTPRGEQVPP---VPS 227  
 DB 597 MPRPMASVVRLLPGSVIAPMPRIIHAPRINVVMPSPAPPIAPMPRPPMIVPAFVAPAP 656

RESULT 7  
 TNC\_MOUSE  
 ID TNC\_MOUSE STANDARD; PRT; 415 AA.

AC P50284;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.  
 GN LTBR OR TNECR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NC NCBITaxID=10090;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-CVB: TISSUE=Lung;  
 MEDLINE=96072804; PubMed=7594541;  
 RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,  
 RA Browning J.U., Ware C.F.;  
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,  
 RT and expression.";  
 RT J. Immunol. 155:5280-5288(1995).  
 RN [2]

RP SEQUENCE FROM N.A.  
 MEDLINE=96163885; PubMed=8586432;  
 RA Nakamura T., Tashiro K., Nakano T., Sasayama S.,  
 RA Honjo T.;  
 RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal  
 RT sequence trap and chromosomal mapping.";  
 RT Genomics 30:312-319(1995).  
 CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN  
 CC IMMUNE DEVELOPMENT.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: U29173; AAA68964.1; -  
 DR EMBL: L38423; AAB00846.1; -  
 DR EMBL: U30798; AAB134.1; -  
 DR HSSP: P25942; 1CDF.  
 DR MGD: MGI:104875; Ltbr  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00020; TNFR\_c6; 3.  
 DR Prodom: PD000771; TNFR\_c6; 1.  
 DR SMART: SM00208; TNFR; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS00500; TNFR\_NGFR\_2; 3.  
 DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
 KW SIGNAL.  
 FT CHAIN 1 30  
 FT DOMAIN 31 415  
 FT DOMAIN 31 223  
 FT TRANSMEM 224 244  
 FT DOMAIN 245 415  
 FT DOMAIN 42 213  
 FT REPEAT 42 81  
 FT REPEAT 82 124  
 FT REPEAT 125 170  
 FT REPEAT 171 213  
 FT DISULFID 43 58  
 FT DISULFID 59 72  
 FT DISULFID 62 80  
 FT DISULFID 83 98  
 FT DISULFID 101 116  
 FT DISULFID 104 124  
 FT DISULFID 126 132  
 FT DISULFID 139 150  
 FT DISULFID 142 169  
 FT DISULFID 172 187  
 FT CARBOHYD 40 40  
 FT CARBOHYD 179 179  
 SO SEQUENCE 415 AA: 44956 MW: 298326A566AEF661 CRC64;

Query Match 7.08; Score 87.5; DB 1; Length 415;  
 Best Local Similarity 24.4%; Pred. No. 2.9;  
 Matches 39; Conservative 20; Mismatches 52; Indels 49; Gaps 8;

QY 110 KCAFPQPPSCL-----RFV-----QTNISRLQETSOLVALKPMITRONFS 151  
 DB 123 ECRQCPGMSCVYLDNCEVHCEERLYLCQPTAEVYDEIMDVNCPCKPGHPTSS 182  
 QY 152 RCLQLQCPDSSSTLPWPSPRPLEATAP-----TAPQPLLLLLPYGLL--- 198  
 DB 183 P--RARQPHTRC-----EIQGLVEAPGTSYSDTICKNPPRGAMLLAILSLVFL 235  
 QY 199 ----LAAWCLHMQRTR-----RRTPRGEQVPPVPSQ 228  
 DB 236 FTVYVLACAMMRHPSLCKRLGLTLKRHPE-GEESPCCAPR 274

RESULT 8  
 MPID\_DROME  
 ID MPID\_DROME STANDARD; PRT; 479 AA.  
 AC P20483; Q9VAL9;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE M-PHASE INDUCER PHOSPHATASE (EC 3.1.3.48) (STRING PROTEIN) (CDC25-LIKE  
 DE PROTEIN).  
 GN SFG OR CDC25 OR CG1395.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NC NCBITaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 MEDLINE=89195217; PubMed=2702688;  
 RA Edgar B.A., O'Farrell P.H.;

RT "Genetic control of cell division patterns in the Drosophila embryo.";  
 RL Cell 57:177-187(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-9106056; PubMed-2120044;  
 RA Jimenez J., Aliphey L., Nurse P., Glover D.M.;  
 RT "Complementation of fission yeast cdc2ts and cdc25ts mutants  
 identifies two cell cycle genes from Drosophila: a cdc2 homologue and  
 string";  
 RL EMO J. 9:3565-3571(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE-20196006; PubMed-10731132;  
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos J., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunbok B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,  
 RA Fodor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin M., Houston K.A., Howland T.J., Wei M.-H., Ibbegam C.,  
 RA Jaisl M., Kalush F., Karpen G.H., Ke Z., Kenton J.A., Kechum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 CC -1- FUNCTION: THIS PROTEIN FUNCTIONS AS A DOSAGE-DEPENDENT INDUCER IN  
 CC MITOTIC CONTROL. IT IS A TYROSINE PROTEIN PHOSPHATASE REQUIRED FOR  
 CC PROGRESSION OF THE CELL CYCLE. IT MAY DIRECTLY DEPHOSPHORYLATE  
 CC P34(CDC2) AND ACTIVATE THE P34(CDC2) KINASE ACTIVITY.  
 CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =  
 CC PROTEIN TYROSINE + ORTHOPHOSPHATE.  
 CC -1- SIMILARITY: STRONG, TO OTHER SPECIES M-PHASE INDUCER PHOSPHATASE  
 CC AND IN GENERAL TO PROTEIN-TYROSINE PHOSPHATASES.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: M24909: AAA28916.1: -  
 CC EMBL: X57495: CAA40732.1: -  
 CC EMBL: AE003768: AAF56885.1: -  
 CC PIR: A32290: A32290.

DR PIR: S12008; S12008.  
 DR HSSP: P30304: 1025.  
 DR FLYBASE: FBgn0003525; stg.  
 DR InterPro: IPR001751; MPl\_Phoptase.  
 DR InterPro: IPR001763; Rhodanese\_domain.  
 DR Pfam: PF00581; Rhodanese\_1.  
 DR PRINTS: PR00716; MPlPHPTASE.  
 DR SMART: SM00450; RHOD: 1.  
 KW Cell division; Mitosis; Hydrolyase.  
 FT ACT\_SITE 379 379 BY SIMILARITY.  
 FT CONFLICT 228 228 A -> T (IN REF. 1).  
 FT SEQUENCE 479 AA; 54094 MW; 68483F3A285962CC CRC64;  
 SO  
 Query Match 7.0%; Score 87.5; DB 1; Length 479;  
 Best Local Similarity 22.9%; Pred. No. 3.4;  
 Matches 56; Conservative 34; Mismatches 76; Indels 79; Gaps 14;  
 OY 1 MTLAPAMSPPTVLL---LLLSGLSGTQDCSPHSPISDFAVKIRELSDYLLQYV 57  
 DB 72 MGLSPESGSPQFQIVROKPIIPANGVS-----DHTPARS-FRI-ENSLSS-----T 117  
 OY 58 VTVASNLQDEELGGLMRLVLAQRMMERLKVAGSKMOGLLEVRVTEIFVTKCAFOPPP 117  
 DB 118 CSMESMSDME-----YMLFEMESQSQ-----QTALGF-----P 146  
 OY 118 SCLRVQVQINISLQDETSEQLVALKP---WTRQNFSCLEL-QCQPPSSTLPWMSRP 173  
 DB 147 SGLN-----SLISQIREQPAKSPAGLSMRPSPVRCLSTESNTSTSTTPPKRPE- 199  
 OY 174 LEATAPFA---POPULLLLLPVGLLLAAMCLMQRTRRRPREQVPPVPSDDL 230  
 DB 200 ---TARDFKREPP-----ASANCSPISKRRKCAVAKENPAPSPISQ 242  
 OY 231 LIVER 235  
 DB 243 VVISH 247  
 RESULT 9  
 DDRI\_RAT STANDARD: PRT; 910 AA.  
 AC Q63474;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE EPITHELIAL DISCOLDIN DOMAIN RECEPTOR 1 PRECURSOR (EC 2.7.1.112)  
 DE (TYROSINE-PROTEIN KINASE CAK) (CELL ADHESION KINASE) (TYROSINE KINASE  
 DE DDR) (DISCOLDIN RECEPTOR TYROSINE KINASE) (PROTEIN-TYROSINE KINASE  
 DE PTK-3).  
 CN DDRI OR EDDRI OR PTK3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain;  
 RX MEDLINE-94173920; PubMed-812787;  
 RA Sanchez M.P., Tapley P., Saini S.S., He B., Pulido D., Barbacid M.;  
 RT "Multiple tyrosine protein kinases in rat hippocampal neurons:  
 RT isolation of Ptk-3, a receptor expressed in proliferative zones of  
 RT the developing brain.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:1819-1823(1994).  
 CC -1- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND  
 CC RECOGNITION (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +  
 CC PROTEIN TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: VARIOUS EMBRYONIC AND ADULT TISSUES; ALSO  
 CC PROLIFERATIVE ZONES OF THE DEVELOPING BRAIN; HIPPOCAMPAL NEURONS.  
 CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF TYR-PROTEIN  
 CC KINASES.



```

CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -----
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CC -----
DR EMBL: L26525; AAA21089.1; -.
DR HSSP: P11362; 1FG1.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000421; FA58_C.
DR InterPro: IPR002011; Reptor_Tyr_kin_II.
DR InterPro: IPR001245; Tyr_kin.
DR Pfam: PF00754; F5_F8_type_C; 1.
DR Pfam: PF00659; pkinase; 1.
DR SMART: SM00231; FA58C; 1.
DR SMART: SM00219; Tyrc; 1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
DR PROSITE: PS01285; FA58C_1; 1.
DR PROSITE: PS01286; FA58C_2; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Tyrosine-protein kinase; Glycoprotein; Signal;
DR Phosphorylation; Transmembrane; Receptor; ATP-binding.
FT CHAIN 1 19
FT DOMAIN 20 910
FT TRANSMEM 414 440
FT DOMAIN 441 910
FT DOMAIN 32 186
FT FT 378 412
FT DOMAIN 473 598
FT DOMAIN 607 902
FT NP_BIND 613 621
FT BINDING 652 652
FT ACT SITE 763 763
FT DISULFID 32 186
FT MOD_RES 510 510
FT MOD_RES 789 789
FT MOD_RES 793 793
FT MOD_RES 794 794
FT CARBOHYD 212 212
FT CARBOHYD 261 261
FT CARBOHYD 371 371
FT CARBOHYD 391 391
SQ SEQUENCE 910 AA; 101164 MW; 7E7FFAIDCB029806 CRC64;

Query Match 7 0%; Score 87; DB 1; Length 910;
Best Local Similarity 24.5%; Pred. No. 8;
Matches 38; Conservative 12; Mismatches 35; Indels 70; Gaps 9;

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ID DDRL_MOUSE STANDARD; PRT; 911 AA.
AC Q03146;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE EPITHELIAL DISCOLDIN DOMAIN RECEPTOR 1 PRECURSOR (EC 2.7.1.112)
DE (TYROSINE-PROTEIN KINASE CAK) (CELL ADHESION KINASE) (TYROSINE KINASE
DE DOR) (DISCOLDIN RECEPTOR TYROSINE KINASE) (PROTEIN-TYROSINE KINASE
DE MK-6).
GN DDRL OR EDDRL OR CAK OR MPK6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=C57BL.
RX MEDLINE=96204002; PubMed=8622863;
RA Perez J.L., Jing S.Q., Wong T.W.;
RT "Identification of two isoforms of the Cak receptor kinase that are
RT coexpressed in breast tumor cell lines.";
RL Oncogene 12:1469-1477(1996).
[2]
RP SEQUENCE OF 766-822 FROM N.A.
RC STRAIN=C57BL; TISSUE=Embryonic brain;
RX MEDLINE=93096484; PubMed=1281307;
RA Gillardi-Hebensstreit P., Nieto M.A., Frain M., Mattei M.-G.,
RA Chastier A., Wilkinson D.G., Charney P.;
RT "An Eph-related receptor protein tyrosine kinase gene segmentally
RT expressed in the developing mouse hindbrain.";
RL Oncogene 7:2499-2506(1992).
CC -1- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND
CC RECOGNITION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CAK I (SHOWN HERE) AND CAK II;
CC ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER BY THE
CC ABSENCE OF A 37 RESIDUES SEGMENT.
CC -1- TISSUE SPECIFICITY: THE PREDOMINANT ISOFORM CAK I, IS EXPRESSED IN
CC DEVELOPING EMBRYO AND ADULT BRAIN; CAK II IS EXPRESSED IN VARIOUS
CC EPITHELIAL CELLS.
CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF TYR-PROTEIN
CC KINASES.
CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L57509; AAB05209.1; -.
DR EMBL: X57240; CAA40516.1; -.
DR PIR: S30502; S30502.
DR HSSP: P11362; 1FG1.
DR MGD: MGI:99216; Ddrl.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000421; FA58_C.
DR InterPro: IPR002011; Reptor_Tyr_kin_II.
DR InterPro: IPR001245; Tyr_kin.
DR Pfam: PF00754; F5_F8_type_C; 1.
DR Pfam: PF00659; pkinase; 1.
DR SMART: SM00231; FA58C; 1.
DR SMART: SM00219; Tyrc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_APP; FALSE_NEG.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.

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DR PROSITE: PS01285; FA58C.1; 1.  
 DR PROSITE: PS01286; FA58C.2; 1.  
 KM Transferase: Tyrosine-protein kinase: Glycoprotein: Signal;  
 KM Phosphorylation: Transmembrane: Receptor: ATP-binding;  
 KM Alternative splicing.  
 FT SIGNAL 1 19  
 FT CHAIN 20 911  
 FT DOMAIN 20 414  
 FT TRANSMEM 415 441  
 FT DOMAIN 442 911  
 FT DOMAIN 32 186  
 FT DOMAIN 379 413  
 FT DOMAIN 474 599  
 FT DOMAIN 608 903  
 FT NP\_BIND 614 622  
 FT BINDING 653 653  
 FT ACT\_SITE 764 764  
 FT DISULFID 32 186  
 FT MOD\_RES 511 511  
 FT MOD\_RES 790 790  
 FT MOD\_RES 794 794  
 FT MOD\_RES 795 795  
 FT CARBOHYD 213 213  
 FT CARBOHYD 262 262  
 FT CARBOHYD 372 372  
 FT CARBOHYD 392 392  
 FT VARSPLIC 503 539  
 FT SEQUENCE 911 AA: 101160 MW: DBB/FE03DD/9510 CRC64;

POTENTIAL.  
 EPITHELIAL DISCOIDIN DOMAIN RECEPTOR 1.  
 EXTRACELLULAR (POTENTIAL).  
 POTENTIAL.  
 CYTOPLASMIC (POTENTIAL).  
 F5/8 TYPE C (PHOSPHOLIPID-BINDING, POTENTIAL).  
 GLY/PRO-RICH.  
 GLY/PRO-RICH.  
 PROTEIN KINASE.  
 ATP (BY SIMILARITY).  
 ATP (BY SIMILARITY).  
 BY SIMILARITY.  
 BY SIMILARITY.  
 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 MISSING (IN ISOFORM CAK II).  
 MISSING (IN ISOFORM CAK II).

Query Match 7.0%; Score 87; DB 1; Length 911;  
 Best Local Similarity 24.5%; Pred. No. 8;  
 Matches 38; Conservative 12; Mismatches 35; Indels 70; Gaps 9;

QY 143 PWITQNSRCLQCPDSSTLP-PW---SPRPLEATA---PTAPQ-----184  
 DB 357 PWLSEISFISDV-VNDSDFPPAPWPPGPPTNFSLEPRGQPVAKAEGSPTA 415  
 QY 185 -----PLLLLLLPVGLLLAAMCHWQ---TRR-----T 214  
 DB 416 ILIGLVAILLLLLLIALML---WRLMRLLSKAEKRVLEELTVHLSVPGDTILIN 471  
 QY 215 PRGEQVPP-----VPSPODLL 232  
 DB 472 NRPGERPPPPYQPRRPRGPPHSAFCVPGSALL 506

RESULT 11  
 ID CNCG4\_BOVIN STANDARD: PRT: 1394 AA.  
 AC 028181: 028082: 003861:  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE 240 KDA PROTEIN OF ROD PHOTORECEPTOR CNCG-CHANNEL (CONTAINS: GLUTAMIC ACID-RICH PROTEIN (GARP): CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4 (CNG CHANNEL 4) (CNG-4) (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL MODULATORY SUBUNIT)).  
 DE CNGB1 OR CNCG4.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RP MEDLINE=96009859; PubMed=7546742;  
 RA Koerschen H.G., Illing M., Seifert R., Sesti F., Williams A.,  
 RA Gotes S., Colville C., Mueller F., Dose A., Godde M., Molday L.,  
 RA Kaupp U.B., Molday R.S.;  
 RT "A 240 kDa protein represents the complete beta subunit of the cyclic nucleotide-gated channel from rod photoreceptor.";

RL Neuron 15:627-636(1995).  
 RN [2]  
 RP SEQUENCE OF 454-1394 FROM N.A.  
 RC TISSUE=Retina;  
 RA Biel M., Zong X., Ludwig A., Sauter A., Hofmann F.;  
 RT "Molecular cloning and expression of the modulatory subunit of the cyclic nucleotide-gated cation channel.";  
 RL J. Biol. Chem. 271:6349-6355(1996).  
 RN [3]  
 RP SEQUENCE OF 1-590 FROM N.A.  
 RC TISSUE=Retina;  
 RA Sugimoto Y., Yatsunami K., Tsujimoto M., Khorana H.G., Ichikawa A.;  
 RL Submitted (xxx-1991) to the EMBL/Genbank/DBS databases.  
 CC -1- SUBUNIT: FORMS FUNCTIONAL HETEROLOGIC CHANNELS WITH CNGB3.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: CNCG4 (SHOWN HERE), CNCG4 AND CNCG4E; ARE PRODUCED BY ALTERNATIVE SPLICING. CNCG4 IS BY FAR THE MOST FREQUENT FORM (CNCG4:CNCG4E = 20:2:1) IN TESTIS.  
 CC -1- TISSUE SPECIFICITY: RETINA, TESTIS, KIDNEY, HEART, AND BRAIN.  
 CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: X89626; CAA61769.1; -;  
 CC EMBL: X94707; CAA64367.1; -;  
 CC EMBL: M61185; AAA30536.1; -;  
 CC InterPro: IPR002025; CNG\_membrane.  
 CC InterPro: IPR000595; CNGP\_binding.  
 CC Pfam: PF00914; CNG\_membrane.1.  
 CC Pfam: PF00027; CNGP\_binding.1.  
 CC SMART: SM00100; CNGP.1  
 DR PROSITE: PS00888; CNGP\_BINDING\_1; 1.  
 DR PROSITE: PS00889; CNGP\_BINDING\_2; 1.  
 DR PROSITE: PS00042; CNGP\_BINDING\_3; 1.  
 KM Ionic channel: Ion transport; CAMP-binding; Transmembrane;  
 KM Multigene family; Alternative splicing.  
 FT CHAIN 1 590  
 FT DOMAIN 454 1394  
 FT DOMAIN 1 767  
 FT TRANSMEM 768 786  
 FT DOMAIN 787 800  
 FT TRANSMEM 801 819  
 FT DOMAIN 821 844  
 FT TRANSMEM 845 864  
 FT DOMAIN 865 901  
 FT TRANSMEM 902 924  
 FT DOMAIN 925 968  
 FT TRANSMEM 969 988  
 FT DOMAIN 989 1072  
 FT TRANSMEM 1073 1093  
 FT DOMAIN 1094 1394  
 FT NP\_BIND 1081 1219  
 FT BINDING 1141 1141  
 FT BINDING 1153 1153  
 FT CARBOHYD 1067 1067  
 FT VARSPLIC 515 532  
 FT VARSPLIC 522 530  
 FT VARSPLIC 341 341  
 FT CONFLICT 454 465  
 FT CONFLICT 482 482  
 FT CONFLICT 499 499  
 FT CONFLICT 572 590  
 FT CONFLICT 1283 1283  
 FT CONFLICT 1289 1289

GLUTAMIC ACID-RICH PROTEIN.  
 CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4.  
 CYTOPLASMIC (POTENTIAL).  
 H1 (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 H2 (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 H3 (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 H4 (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 H5 (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 H6 (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 CAMP (BY SIMILARITY).  
 CAMP (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 MISSING (IN ISOFORM CNCG4E).  
 MISSING (IN ISOFORM CNCG4).  
 K -> E (IN REF. 3).  
 REEDEDDEED -> MRGQGRG (IN REF. 2).  
 R -> O (IN REF. 2 AND 3).  
 A -> T (IN REF. 3).  
 VPAIEHPLEQVDDADS -> GSPQSPFPALEQCEALK  
 R (IN REF. 3).  
 S -> A (IN REF. 2).  
 R -> A (IN REF. 2).





DT 15-DEC-1998 (Rel. 37, last sequence update)  
 DT 20-AUG-2001 (Rel. 40, last annotation update)  
 DE MAX BINDING PROTEIN MNT (FOX PROTEIN) (MYC ANTAGONIST MNT).  
 GN MNT OR ROX.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Petal brain;  
 RX MEDLINE=97327566; PubMed=9184233;  
 RA Meroni G., Raymond A., Alcalay M., Borsani G., Tanigami A.,  
 RA Tonlondrenzi R., Lo Nigro C., Messali S., Zollo M., Ledbetter D.H.,  
 RA Brent R., Ballabio A., Carozzo R.;  
 RT "Fox, a novel bHLH2ip protein expressed in quiescent cells that  
 RT heterodimerizes with Max, binds a non-canonical E box and acts as a  
 RT transcriptional repressor.";  
 RL EMBL J. 16:2892-2906(1997).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=98260677; PubMed=9598315;  
 RA Nigro C.L., Venesio T., Raymond A., Meroni G., Alberici P.,  
 RA Cainerca S., Enrico F., Stack M., Ledbetter D.H., Liscia D.S.,  
 RA Ballabio A., Carozzo R.;  
 RT "The human ROX Gene: genomic structure and mutation analysis in human  
 RT breast tumors.";  
 RL Genomics 49:275-282(1998).  
 CC -1- FUNCTION: BINDS DNA AS A HETERODIMER WITH MAX AND REPRESSES  
 CC TRANSCRIPTION. BINDS TO THE CANONICAL E BOX SEQUENCE  
 CC 5'-CACGCG-3' AND, WITH HIGHER AFFINITY, TO 5'-CACGCC-3'.  
 CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER  
 CC BHLH PROTEIN. BINDS DNA AS AN HOMODIMER OR A HETERODIMER WITH MAX.  
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
 CC TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
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 CC -----  
 DR EMBL: X96401; CAA65265.1; -;  
 DR EMBL: Y13440; CAA73851.1; -;  
 DR EMBL: Y13441; CAA73851.1; JOINED.  
 DR EMBL: Y13442; CAA73851.1; JOINED.  
 DR EMBL: Y13443; CAA73851.1; JOINED.  
 DR EMBL: Y13444; CAA73851.1; JOINED.  
 DR EMBL: Y13444; CAA73851.1; JOINED.  
 DR MIM: 603039; -;  
 DR InterPro: IPR003015; HLH\_Myc.  
 DR InterPro: IPR001092; HLH\_dlm.  
 DR Pfam: PF00010; HLH\_1.  
 DR SMART: SM00353; HLH\_1.  
 DR PROSITE: PS00038; HELIX\_LOOP\_HELIX; FALSE\_NEG.  
 KW Transcription regulation; Repressor; Nuclear protein; DNA-binding.  
 FT DNA\_BIND 222 233 BASIC DOMAIN.  
 FT DOMAIN 234 270 BASIC DOMAIN.  
 FT DOMAIN 271 299 LEUCINE-ZIPPER.  
 SO SEQUENCE 582 AA; 62299 MW; 06AC320D79BF18A0 CRC64;

Query Match 6.88; Score 84; DB 1; Length 582;

Best Local Similarity 21.18; Pred. No. 8.5; Mismatches 89; Indels 104; Gaps 13;

OY 4 LAPAWSTTYLLLLLS-----GLSGTQDCSFQHSPISSDPAVKIRELSDY 51  
 Db 186 LAPQPPPTLGLTKLAPAEVKSSEQKRRPGIGTREV---HNKLEKNRRRAHLKECFET 242  
 OY 52 FLQDYPTVASNLODELGGLMRLVLAQRMEKLTIVAGSKMGLLERVNTEIHFVTKC 111

Db 243 LKRNP-----MDDK-TSNLSVLRTPALRYIOSLKR-KEKEYEHMERLARE-----KI 290  
 OY 112 AFQPPSCLEFVQTNISRLLOETSEQLVALKPMTRQNFSCLELOCPD----- 161  
 Db 291 A-----TOORLAEHLHLSO-----WMDVLEIDRVLRQTOQPEDDASTAS 333  
 OY 162 -----SSTLPPP-MSRPLEATAPAPQPLLL 189  
 Db 334 EGEDNIDEMEDRAGLGPPLKLSHRPQPELLKSTLPPSTPAPL-----PPHPPH----- 385  
 OY 190 LLPLVGLLLAAAMCLMQRTRRTTPRGEVPP-----VSPQDL 231  
 Db 386 ---PHSVALLPPLHLVQOQOPQKTPLPAPPPPAAPQTLVPAHVLV 431

Search completed: April 1, 2002, 06:27:05  
Job time: 626 sec

Mon Apr 1 06:15:19 2002

us-08-162-407-6.rsp

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Db 181 APOAPRLILLLLPVALLLMSTAMCLHWRRRRRRSPYGEORITLRPSESHLPED 236

# RESULT 2

09MZU9 PRELIMINARY; PRT; 291 AA.

AC 09MZU9

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE FLU3 LIGAND.

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI\_TaxID=9685;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-20358731; PubMed=10902925;

RA Yang S., Sim G.K.;

RT "Molecular cloning of canine and feline flt3 ligand reveals high

RT degree of similarity to the human and mouse homologue but uniquely

RT long cytoplasmic domain."

RL DNA Seq. 11:163-166(2000).

DR EMBL: AF155149; AAF87089.1; -

SO SEQUENCE 291 AA; 32459 MW; 8F85A10A5EA0DCC6 CRC64;

Query Match 72.0%; Score 894.5; DB 6; Length 291;

Best Local Similarity 80.5%; Pred. No. 8.1e-77;

Matches 178; Conservative 9; Mismatches 33; Indels 1; Gaps 1;

QY 1 MTVLAPAMSPPTTLLSSGSGTDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60

Db 1 MTVLAPAMSPPTTLLSSGSGTDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60

QY 61 ASNLODEELCGMLRVLAORMMERLKTAVAGSKMOGLLEVNTEIHFVTKCAFQPPESC 120

Db 61 ASNLODEELCGMLRVLAORMMERLKTAVAGSKMOGLLEVNTEIHFVTKCAFQPPESC 120

QY 121 RFVOTNISRLQETSEOLVALKFWITRONFSRCLELQCPDSSSTLPWPSPRPLEATAP 180

Db 121 RFVOTNISRLQETSEOLVALKFWITRONFSRCLELQCPDSSSTLPWPSPRPLEATAP 180

QY 181 APOAPRLILLLLPVALLLMSTAMCLHWRRRRRRSPYGEORITLRPSESHLPED 220

Db 181 APOAPRLILLLLPVALLLMSTAMCLHWRRRRRRSPYGEORITLRPSESHLPED 221

RESULT 3

09GKED PRELIMINARY; PRT; 292 AA.

AC 09GKED

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DE FLU3 LIGAND ISOFORM-1.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed-11120823;

RA Mwangi W., Brown W.C., Palmer G.H.;

RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain

RT required for receptor binding and function using naturally occurring

RT ligand isoforms."

RL J. Immunol. 165:6966-6974(2000).

DR EMBL: AF282985; AAF9322.1; -

SO SEQUENCE 292 AA; 32390 MW; D68B9ED79221202D CRC64;

Query Match 67.6%; Score 840; DB 6; Length 292;

Best Local Similarity 76.3%; Pred. No. 1.2e-71;

Matches 171; Conservative 12; Mismatches 37; Indels 4; Gaps 2;

QY 1 MTVLAPAMSPPTTLLSSGSGTDCSFQHSPISSDFAVKIRELSYLLQDYPVT 59

Db 1 MTVLAPAMSPPTTLLSSGSGTDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60

QY 60 VASNLODEELCGMLRVLAORMMERLKTAVAGSKMOGLLEVNTEIHFVTKCAFQPPESC 119

Db 61 VASNLODEELCGMLRVLAORMMERLKTAVAGSKMOGLLEVNTEIHFVTKCAFQPPESC 120

QY 120 LRFVOTNISRLQETSEOLVALKFWITRONFSRCLELQCPDSSSTLPWPSPRPLEATAP 179

Db 121 LRFVOTNISRLQETSEOLVALKFWITRONFSRCLELQCPDSSSTLPWPSPRPLEATAP 180

QY 180 TAPQPP---LLLLLPVGLLLAAMCLHWRRRRRRTPRPEQ 220

Db 181 PGQSPILLLLPVALLLMSTAMCLHWRRRRRRTPRPEQ 224

RESULT 4

09GKED PRELIMINARY; PRT; 274 AA.

AC 09GKED

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DE FLU3 LIGAND ISOFORM-2.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed-11120823;

RA Mwangi W., Brown W.C., Palmer G.H.;

RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain

RT required for receptor binding and function using naturally occurring

RT ligand isoforms."

RL J. Immunol. 165:6966-6974(2000).

DR EMBL: AF282986; AAF9323.1; -

SO SEQUENCE 274 AA; 30372 MW; 725A7F77A95DA98B CRC64;

Query Match 60.1%; Score 746; DB 6; Length 274;

Best Local Similarity 69.6%; Pred. No. 8.6e-63;

Matches 156; Conservative 12; Mismatches 34; Indels 22; Gaps 3;

QY 1 MTVLAPAMSPPTTLLSSGSGTDCSFQHSPISSDFAVKIRELSYLLQDYPVT 59

Db 1 MTVLAPAMSPPTTLLSSGSGTDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60

QY 60 VASNLODEELCGMLRVLAORMMERLKTAVAGSKMOGLLEVNTEIHFVTKCAFQPPESC 119

Db 61 VASNLODEELCGMLRVLAORMMERLKTAVAGSKMOGLLEVNTEIHFVTKCAFQPPESC 114

QY 120 LRFVOTNISRLQETSEOLVALKFWITRONFSRCLELQCPDSSSTLPWPSPRPLEATAP 179

Db 115 -----QDTHOLELAKFWITRONFSRCLELQCPDSSSTLPWPSPRPLEATAP 162

QY 180 TAPQPP---LLLLLPVGLLLAAMCLHWRRRRRRTPRPEQ 220

Db 163 PGQSPILLLLPVALLLMSTAMCLHWRRRRRRTPRPEQ 206

# RESULT 5

061104 PRELIMINARY; PRT; 172 AA.

AC 061104

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)



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DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE FL13 LIGAND, T169 FORM.
GN FL13L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K.,
RA Matsun T., Tsai S., Luh J., Guimares M.J., Mattei M.G., Rosnet O.,
RA Birnbaum D., Hannum C.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U44024; AAA93305.1; -.
DR MGI: 95560; Flt3l.
SO SEQUENCE 172 AA; 19465 MW; 04FA0A01071E3384 CRC64;

Query Match 48.5%; Score 602.5; DB 11; Length 172;
Best Local Similarity 72.6%; Pred. No. 2e-49;
Matches 122; Conservative 15; Mismatches 28; Indels 3; Gaps 2

OY 1 MTVALPAMSP-TTYLLLLLLSSGISTDDCSFQHSPISSDPAVKIRLSDYLLDYPVT 59
    ||||| : ||||| | | | | | | | | | | | | | | | | | | | |
DB 1 MTVALPAMSPNSLLLLLLSPCCRGTPDCYFHSPISSNFKVYFRELTDHLKDPVT 60
    ||||| : ||||| | | | | | | | | | | | | | | | | | | | |
OY 60 VASNIODELFCGLRLVLAORWMERLKTAVASKMOGLIERVNTFHEPTKCAFPSPSC 119
    ||||| : ||||| | | | | | | | | | | | | | | | | | | | |
DB 61 VAVNIODEKHCALMSLELAQWRIEQLKTAVASKMOTLLIEDYNTLHFVTSCTFPDLPFC 120
    ||||| : ||||| | | | | | | | | | | | | | | | | | | | |
OY 120 LRFVQTNISRLQETSEQLVALKPWITR-QNFSRCLQLQCPDSSSTL 165
    ||||| : ||||| | | | | | | | | | | | | | | | | | | | |
DB 121 LRFVQTNISHLKDTCTQLALPKPCIGKACQNFSCRLEVOQCPDRVSL 168
    ||||| : ||||| | | | | | | | | | | | | | | | | | | | |

RESULT 6
O9LGC8 PRELIMINARY; PRT; 579 AA.
O9LGC8 AC
O9LGC8:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PURATIVE EXTENSIN-LIKE PROTEIN.
GN P0406H10.6 OR OJ1174_D05.5.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0406H10."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, BAC
RT clone:OJ1174.D05."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF002524; BAB07956.1; -.
DR EMBL: AP003118; BAB33013.1; -.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR002965; P_fich_extensn.
DR InterPro: IPR000504; RM.
DR Pfam: PF00560; LRR; 2.
DR PRINTS: PR01217; PRICHEXTENSN.
DR SMART: SM00370; LRR; 5.
DR PROSITE: PS00030; RRM_RNP_1; UNKNOWN_1.

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SQ      SEQUENCE    579 AA;   62607 MW;   04457E18E7405AA PRC64;

Query Match          9.1%; Score 112.5; DB 10; Length 579;
Best Local Similarity 23.7%; Pred. NO. 0.018;
Matches     54; Conservative         28; Mismatches       69; Indels        77; Gaps           11;

QY      LLLLLSSGLSTGDCSFHSPISSDFAVKIRELSIDYLDDYPVTASNLDDELCSGLMRL 76
DB      :|::||| |               : :: ||| : 
244 ILLINTGS-----SCLPPEGM-LRETVF-----DVSFNRIAGLPISA 282
QY      VLAQRMEELKTVASKMOGLEVRNTEHFYTCAFO-----PPSCLRV-----QT 125
DB      |:|::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |
283 VAGMRVEQL-DVAHNHLTGALPAQCVELPRLNFTFAVNFEETGEPPSCAHAVPYRGDR 341
QY      126 NI--SRILDETSEOLVALKPWITRONFSR---CLELOCOPDSLTLPWPMSRPLEATAP 179
DB      : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
342 NCLPNRPARTIRLOACA*------FAHPYNCAAFQCKPFVPVALPPPSPPP- -SRPP 391
QY      180 TARPDPRLLLLIPVGILLLAAACLHMORTRRTPRPGEQVPPVSP 227
DB      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
392 PSPPP-----SPPPTSPPPSP 411

RESULT      7
Q9DWB8 ID Q9DWB8 PRELIMINARY; PRY: 1240 AA.
AC Q9DWB8;
DT 01-MAR-2001 (TREMBREL. 16, Created)
DT 01-MAR-2001 (TREMBREL. 16, Last sequence update)
DE 01-MAR-2001 (TREMBREL. 16, Last annotation update)
PR2.
R2.
OS Rat cytomegalovirus (strain Mastricht).
OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Muromegalovirus.
OX NCBI_TaxId=79700;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MASTRICHT;
RX MEDLINE=20366325; PubMed=10906222;
RA Vink C., Beuken E., Bruggeman C.A.;
RT "Complete DNA sequence of the rat cytomegalovirus genome.";
RL J. Virol. 74:7656-7665(2000).
RM [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MASTRICHT;
RX MEDLINE=20473137; PubMed=11018281;
RA Gruijthuisen Y.R., Beuken E., Bruggeman C.A., Vink C.;
RT "Rat cytomegalovirus R89 is a highly conserved gene which expresses a
spliced transcript.";
RL Virus Res. 69:119-130(2000);
DR EMBL: AF232689; AAF99111.1; -.
SQ SEQUENCE 1240 AA; 125612 MW; 33BC13DC6A27ZB0 CRC64;

Query Match          7.7%; Score 95.5; DB 12; Length 1240;
Best Local Similarity 33.0%; Pred. NO. 1.7;
Matches     29; Conservative         8; Mismatches       18; Indels        33; Gaps            5;

QY      160 PSSSTL-----PPWSRP.-LEATAAPAQP-PDLLLLPVGLLLAA 201
DB      |||||| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |
1060 PSSSAVTGEATTERSTATERPRPLCPGVDSLALPALPQGIFTLLSLTLVA----- 1112
QY      202 AMCLHMORTRKTTPRPGEQVPPVSP 229
DB      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
1113 -----CATRASPRETDAPP-PPPAD 1132

RESULT      8
Q9C5T0 ID Q9C5T0 PRELIMINARY; PRY: 658 AA.
AC Q9C5T0;
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Db 76:PPGPPRLPCSGSTPPGRLLPQ-----ALAPQGHGESS--RFWEHPTTQAPPPG 127
OY 170 SPRPL-EATAP-----TAPQPLLLLLPVGLLLAAACLMQRRRTPRPG 218
    ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 128 PPRPLPQALVPPQDHGSSPRTQAPPL-----W-LHPRTT--OTPPPG 169
OY 219 EQVPPVSPQDL-LVEH 235
    || | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 170 ---PPRPLPQALPQLQDH 164

RESULT 11
O9PU36
ID O9PU36 PRELIMINARY: PRT: 5120 AA.
AC O9PU36:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ACZONIN (FRAGMENT).
GN ACZ.
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99439764; PubMed=1050862;
RA Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,
RA Killmann M.W.;
RT "Aczonin, a 550-kd putative scaffolding protein of presynaptic active
RT zones, shares homology regions with rim and bassoon and binds
RT profilin.";
RL J. Cell Biol. 147:151-162(1999).
DR EMBL: Y19187; CAB60725.1; -.
DR HSSP: P04410; 1A25.
DR InterPro: IPR000008; C2.
DR InterPro: IPR001478; PDZ.
DR InterPro: IPR002965; P-rich_extensn.
DR InterPro: IPR001565; Synaptotagmin.
DR Pfam: PF00168; C2; 2.
DR Pfam: PF00595; PDZ; 1.
DR PRINTS: PRO0360; C2DOMAIN.
DR PRINTS: PRO1217; PRICHEXTENS.
DR PRINTS: PRO0399; SYNAPTOTAGM.
DR SMART: SM00239; C2; 2.
DR SMART: SM00228; PDZ; 1.
DR PROSITE: PS00499; C2_DOMAIN_1; UNKNOWN_1.
DR PROSITE: PS00004; C2_DOMAIN_2; 2.
DR PROSITE: PS50106; PDZ; 1.
DR NON_TER
FT
SQ SEQUENCE 5120 AA; 560760 MW; A658D9891B65B412 CRC64;
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Db 2403 PPKPS 2407

RESULT 12
ID 017610 PRELIMINARY: PRT: 474 AA.
AC 017610:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE C28D4.2 PROTEIN.
GN C28D4.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilita; Rhabdilitidae;
OC Rhabdilitae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurtry A.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z82259; CAB05129.1; -.
DR InterPro: IPR002573; Choline_kinase.
DR Pfam: PF01633; Choline_kinase; 1.
SQ SEQUENCE 474 AA; 54628 MW; DDF1IC97A1542FFC CRC64;

Query Match 7.2%, Score 89.5; DB 5; Length 474;
Best Local Similarity 24.1%, Pred. No. 2.2;
Matches 59; Conservative 29; Mismatches 82; Indels 75; Gaps 15;

OY 27 TQDC-----SFQHS-PISDFAVKIREL-SDYLQDYPTVASNLQDEELCGLWRL 76
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 65 TTDCVDLKKVFESKFPSSAPISSEILFRARFLCAKL-----CGARRK 106
OY 77 VLAQRMERLKTAVAGSKQGLLERVNTIEHYTKCAFQPPPSCLR-FYQFNISRLQET- 134
    | : : : : | | | | | | | | | | | | | | | | | | | | | |
Db 107 VKIEEF--RIRAITGG-KSNLLFLVELPAH-LTPIQMEPEKALLHVHCQSDIDQLSESV 162
OY 135 -----SQQLAALKPWITRQMFNSRCLQCC-----QPDSTLPPPMSPR--PLEATA 178
    : : : : : | | | | | | | | | | | | | | | | | | | | | |
Db 163 VETLLSERNLGPKMLGVPPGREFQFIPSRALQCEISPGSLIAPIVAVVHTLDAPV 222
OY 179 PTAQPPRLLLLLPVGLLLAAACLMQRRRTPRP--RPGE-----QVPVPSPOD 229
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 223 PKEPQ-----TLQTRQWLRF-----KKTFRAGERIEMYLQAKVPKSDYFST 266
OY 230 LLIVE 234
    : : :
Db 267 ITVAQ 271

RESULT 13
O9UMT1
ID O9UMT1 PRELIMINARY: PRT: 270 AA.
AC O9UMT1:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE NKp44RG2 PROTEIN.
GN NKp44RG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RC Cantoni C., Biasoni R.;
RT "NKp44 related genes.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AJ010100; CAB52290.1; -.
```

DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00409; Ig; 1.  
 SO SEQUENCE 270 AA; 29678 MW; 327AD57A5634AE46 CRC64;

Query Match 7.1%; Score 88.5; DB 4; Length 270;  
 Best Local Similarity 23.0%; Pred. No. 1.5;  
 Matches 63; Conservative 22; Mismatches 112; Indels 77; Gaps 15;

QY 7 AMSGTYLLLLLSGLSGTQDCSPQHSPISSDPAVKIRLSYLLQDYVTVASNLQD 66  
 DB 2 AWRALHPLLLLLEPPSQASQAKVUQSVAGQTLTVRCQ-----YPT----- 45  
 QY 67 EELGGLM-----RLVLAQR-----HMERLKTGSKMOGLLEVRNTEI- 105  
 DB 46 -----GSLYEKKGCKEASALVCILVYSSKPRMAMWTSRF-TIMDDDAGCFYTMIDL 100  
 QY 106 -----HFVTKCAFQPPSCLEFVQTNISRLQETSEQLVAKPWITRONFSRCLQLQ-CQ 159  
 DB 101 EEDSGHY--MCRIYRPSD--NSVSKSVREYLVSPASASTQTPTWPRDLVSSQTQFQSCV 156  
 QY 160 PDS-----STLPPMSP-RELENTAPTAQ-----PPLLLLLLPV--GLL-- 197  
 DB 157 PPTAGAHQAPSPSTIVPSHPSPLEVPSPRPNSTLRPPGAPALVLPVFCGLLVAK 216  
 QY 198 -LLAAACLHMORTRRTPRPEQV--PPVSPQ 228  
 DB 217 SLVSLALLVWVVLNRHMHGRLHPAQRPO 250

RESULT 14  
 Q9AMJ4 PRELIMINARY; PRT; 404 AA.  
 ID 09AMJ4:  
 AC 09AMJ4:  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE P0489A05.3 PROTEIN.  
 GN P0489A05.3.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Erihartoideae; Oryzaceae; Oryza.  
 OC NCBI\_TaxID=4530;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=CV. NIPPONBARE;  
 RC SASAKI T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC  
 clone;P0489A05.";  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AP003105; BAB32983.1; -  
 SO SEQUENCE 404 AA; 43109 MW; 7CA66FDE772A4B CRC64;

Query Match 7.1%; Score 88.5; DB 10; Length 404;  
 Best Local Similarity 26.1%; Pred. No. 2.3;  
 Matches 66; Conservative 24; Mismatches 88; Indels 75; Gaps 17;

QY 33 QHSPISSDF--AKVIRELSYLLQDYVTVASNL-----ODEELGGLMRLVL 78  
 DB 107 RHFSLSEFLEKVOITPLKYVSMNYPLKPNQTFLLNRYQMKNSPEQLCKRFW---- 162  
 QY 79 AQRMEELKTVAGSKMG-----LLERVNT--EIHVTKCAFQPPSCLEFVQTNI--SRL 130  
 DB 163 -STWQSNAGAV-GSRAGSERLRLRPSSAGRRPWLVPSPPPRASLAAGVYNALTSRA 220  
 QY 131 LOETSEQLVAKPWITRONFSR--CLELQ--CQDPSSTLP-----PPWSRPLEAT 177  
 DB 221 LSAATG-----TPTTSSSILRRPLHCLLPLRLARPSPSPILPLQAPRHPPLP---P 271

QY 178 APTAPQPELLLLLL-----PV---GLL-----LLAAACLHMORTRRTPR 216  
 DB 272 PPTARAPPVIAVLCILRCPLYPKRPVAGGLFVAHSALTAVLCAGGCV--RRLHRRPLR 329  
 QY 217 P--GEQVPPVPS 227  
 DB 330 PPSELLPLSRAP 342

RESULT 15  
 075064 PRELIMINARY; PRT; 1386 AA.  
 ID 075064:  
 AC 075064:  
 DT 01-NOV-1998 (Tremblrel. 08, Created)  
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
 DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE KIAA0476 PROTEIN.  
 GN KIAA0476.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE=98116662; PubMed=9455484;  
 RA Seki N., Ohira M., Nagase T., Ishikawa K., Miyajima N., Nakajima D.,  
 RA Nomura N., Ohara O.;  
 RT "Characterization of cDNA clones in size-fractionated cDNA libraries  
 from human brain.";  
 RL DNA Res. 4:345-349(1997).  
 DR EMBL: AB007945; BAA32321.1; -  
 DR InterPro: IPR001194; DENN.  
 DR InterPro: IPR002885; PPR.  
 DR Pfam: PF01535; PPR; 1.  
 DR Pfam: PF02141; DENN; 1.  
 SO SEQUENCE 1386 AA; 152296 MW; BE96DE7169A7EFDA CRC64;

Query Match 7.1%; Score 88.5; DB 4; Length 1386;  
 Best Local Similarity 23.1%; Pred. No. 8.6;  
 Matches 53; Conservative 28; Mismatches 85; Indels 63; Gaps 12;

QY 21 SSGLSGTQDCSPQHSPISSDPAVKIRLSYLLQDYVTVASNLQDELC-----GGLMRL 76  
 DB 1104 SAGASGSKDAPVPGP-----GVLSDRLCLA--LDEPOLCNGHMGASRR 1148  
 QY 77 VLAQRMEELKTVAGSKMGGLLEVRNTEIHVTKCAFQPPSCLEFVQTNISRLQETSE 136  
 DB 1149 VESGAMVYLSPLVLRKELESIVENEGSEV-----LALPELSAHPITFWNLMTFORL-- 1201  
 QY 137 QLVAKPWITRONFSRCLQLQDQ--PDSSTLPWPW--SPRPLEA-----TAPTAPQP 185  
 DB 1202 RLPSILPGLVLA-----CQSPSHQAPSPWLTPDPAISVYRLMDVLITDPNCSPP 1253  
 QY 186 LLLILLPVGLLLLAAACLHMORTRRTPRPEQVPPSPDOLLIVE 234  
 DB 1254 LYVL-----WRVHSQ-IPORVWPG---PVPASLSLALLE 1284

Search completed: April 1, 2002, 06:25:43  
 Job time: 619 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2002, 06:13:54 ; Search time 77.69 Seconds  
(without alignments)  
224.060 Million cell updates/sec

Title: US-08-162-407-6

Perfect score: 1242  
Sequence: 1 MTVLAPAWSPPTLYLLLLL.....RPGGVVPVSPDQLLVH 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_1101:\*

1: /SID52/gcgdata/geneseq/geneseq/AA1980.DAT:\*

2: /SID52/gcgdata/geneseq/geneseq/AA1981.DAT:\*

3: /SID52/gcgdata/geneseq/geneseq/AA1982.DAT:\*

4: /SID52/gcgdata/geneseq/geneseq/AA1983.DAT:\*

5: /SID52/gcgdata/geneseq/geneseq/AA1984.DAT:\*

6: /SID52/gcgdata/geneseq/geneseq/AA1985.DAT:\*

7: /SID52/gcgdata/geneseq/geneseq/AA1986.DAT:\*

8: /SID52/gcgdata/geneseq/geneseq/AA1987.DAT:\*

9: /SID52/gcgdata/geneseq/geneseq/AA1988.DAT:\*

10: /SID52/gcgdata/geneseq/geneseq/AA1989.DAT:\*

11: /SID52/gcgdata/geneseq/geneseq/AA1990.DAT:\*

12: /SID52/gcgdata/geneseq/geneseq/AA1991.DAT:\*

13: /SID52/gcgdata/geneseq/geneseq/AA1992.DAT:\*

14: /SID52/gcgdata/geneseq/geneseq/AA1993.DAT:\*

15: /SID52/gcgdata/geneseq/geneseq/AA1994.DAT:\*

16: /SID52/gcgdata/geneseq/geneseq/AA1995.DAT:\*

17: /SID52/gcgdata/geneseq/geneseq/AA1996.DAT:\*

18: /SID52/gcgdata/geneseq/geneseq/AA1997.DAT:\*

19: /SID52/gcgdata/geneseq/geneseq/AA1998.DAT:\*

20: /SID52/gcgdata/geneseq/geneseq/AA1999.DAT:\*

21: /SID52/gcgdata/geneseq/geneseq/AA2000.DAT:\*

22: /SID52/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	16	AA67541 Human flt-3 ligand
2	1242	100.0	235	20	AA67769 Human flt3-ligand
3	1242	100.0	235	21	AA69719 Full length wild t
4	1242	100.0	235	22	AA620192 Human flt-3 ligand
5	1236	99.5	235	16	AA66175 Human S86/s109 flt
6	1236	99.5	235	22	AA620194 Human flt-3 ligand
7	1124	89.7	209	19	AA69721 Human flt-3 recept
8	1114	89.7	209	21	AA69720 Mature wild type h
9	1114	89.4	209	21	AA69723 Human flt-3 mutcin
10	1110	89.4	209	21	AA69726 Human flt-3 mutcin
11	1110	89.4	209	21	AA69726 Human flt-3 mutcin

12	1110	89.4	209	21	AA69727 Human flt-3 mutcin
13	1110	89.4	209	21	AA69729 Human flt-3 mutcin
14	1108	89.2	209	21	AA69722 Human flt-3 mutcin
15	1108	89.2	209	21	AA69724 Human flt-3 mutcin
16	1107	88.6	209	21	AA69728 Human flt-3 mutcin
17	1100	88.6	209	21	AA69725 Human flt-3 mutcin
18	970	78.1	185	22	AA658204 Human flt-3 ligand
19	895.5	72.1	294	21	AA658204 Human flt-3 ligand
20	894.5	72.0	291	21	AA658210 Human flt-3 ligand
21	834	67.1	178	22	AA620193 Human flt-3 ligand
22	797.5	64.2	268	21	AA658206 Human mature flt-
23	796.5	63.7	276	21	AA658207 Canine flt-3 ligand
24	791.5	63.7	265	21	AA658211 Feline mature flt-
25	768.5	61.9	231	16	AA667540 Mouse flt-3 ligand
26	768.5	61.9	231	20	AA667768 Murine flt3-ligand
27	768.5	61.9	231	22	AA620186 Mouse flt-3 ligand
28	768	61.8	232	16	AA66177 Mouse Mot10/T118
29	764	61.5	232	22	AA620189 Mouse flt-3 ligand
30	745	60.0	150	19	AA677930 Flt3 ligand FL10C
31	745	60.0	150	19	AA669054 Human flt-3 recept
32	740.5	59.6	377	19	AA678124 Chimeric receptor
33	739	59.5	143	19	AA677926 Flt3 ligand FL13C
34	739	59.5	143	19	AA669050 Human flt3 ligand
35	737.5	59.4	349	19	AA683289 Human flt3 ligand
36	737.5	59.4	349	19	AA678005 Flt3L 1-139/IG52b/
37	736.5	59.3	340	19	AA683291 Human flt3 ligand
38	736.5	59.3	349	19	AA683286 Human flt3 ligand
39	736.5	59.3	523	19	AA678008 Trimeric Flt3L-G-C
40	735	59.2	140	19	AA677911 Human flt3 ligand
41	735	59.2	140	19	AA669035 Human flt-3 recept
42	735	59.2	144	19	AA677928 Flt3 ligand FL14C
43	735	59.2	144	19	AA669052 Human flt-3 recept
44	735	59.2	313	19	AA683294 Human flt3 ligand
45	733.5	59.1	286	19	AA683303 Human flt3 ligand

#### ALIGNMENTS

RESULT 1	AA67541	standard: Protein: 235 AA.
XX	AA67541:	
AC	AA67541:	
XX	05-AUG-1995 (first entry)	
XX	Human flt-3 ligand.	
DE	Human flt-3 ligand.	
XX	Human flt-3 ligand.	
KW	Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.	
XX	Homo sapiens.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	Peptide	1..26
FT		/label= "Sig.peptide
FT		/note= "signal peptide may extend to position 27"
FT	Domain	27..182
FT		/label= "Extracellular-domain
FT		/note= "extracellular domain may start at
FT		position 28"
FT	Domain	183..205
FT		/label= "Transmembrane-domain
FT	Domain	206..235
FT		/label= "Cytoplasmic-domain
XX	EP627487-A.	
XX	07-DEC-1994.	
XX	19-MAY-1994:	94EP-0303575.
XX	24-MAY-1993:	93US-0068394.

PR 12-AUG-1993; 93US-0106463.  
 PR 25-AUG-1993; 93US-0111758.  
 PR 03-DEC-1993; 93US-0162407.  
 PR 07-MAR-1994; 94US-0209502.  
 PR 11-MAY-1994; 94US-0243545.  
 XX  
 PA (IMMUNEX CORP.  
 XX  
 PI Beckmann MP, Lyman SD;  
 XX  
 DR WPI: 1995-008071/02.  
 DR N-PSDB; AAQ79079.  
 XX  
 PT Isolated ligands for flt 3 receptors - useful for treating  
 PT anaemia, AIDS and various cancers  
 PS  
 XX Disclosure; Page 29-30; 33pp; English.  
 XX  
 CC A human T-cell lambda-gli0 random primed cDNA library was  
 CC screened with a fragment corresponding to the extracellular  
 CC domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AAQ79076)  
 CC to isolate human flt3-L cDNA. Flt-3 stimulates progenitor and  
 CC stem cells, and can be used e.g. in gene therapy protocols.  
 XX  
 SQ Sequence 235 AA;  
  
 Query Match 100.0%; Score 1242; DB 16; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-109;  
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60  
 DB 1 mtvalapawspptyllllllssgsgtqdcsfqhspsdsfavkirelsdyllqdyptv 60  
 QY 61 ASNQDEELCGGLRVLVLAQRWMERLKTVAAGSKKQGLLEVRNTEIHFTVTCARQPPPSCL 120  
 DB 61 asnlqdeelcggglrvlvaqrwmerlktvagskmgllervnteihvtkcatqpppscl 120  
 QY 121 RFVQTNISRLQETSEQLVAKPWITRONFSRCLELCCOPDSSFTLPPWSPRPLEATAPT 180  
 DB 121 rfvtgnisrllqetseqvlakpwitrgnfsrclelccqpdssclppwsprrpleatapt 180  
 QY 181 APQPLLILLLLPVGLLLAAAWCLHWQRTTRRRTPRGEQVPPVPSQDILLVEH 235  
 DB 181 apqpplllllllpvglilllaawclhwgrtrrrtrrpgeqvppvpqdillveh 235  
  
 RESULT 2  
 ID AAM67769 standard; Protein: 235 AA.  
 XX  
 AC AAM67769;  
 XX  
 DT 25-MAR-1999 (first entry)  
 XX  
 DE Human flt3-ligand.  
 XX  
 KW Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L;  
 KW immunogenic; autoimmune disease; organ transplantation; food allergy;  
 KW tissue transplantation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9857655-A1.  
 PD 23-DEC-1998.  
 XX  
 PF 12-JUN-1998; 98WO-US12085.  
 XX  
 PR 17-JUN-1997; 97US-0877421.  
 XX  
 PA (IMMUNEX CORP.

XX  
 PI Abbott NM, Mowat AM, Viney JL;  
 XX  
 DR WPI: 1999-070422/06.  
 DR N-PSDB; AAV81506.  
 XX  
 PT Methods for initiating or enhancing antigen specific immune  
 PT tolerance - by using murine or human flt3 ligand  
 PS  
 XX Claim 1; Page 14-15; 25pp; English.  
 XX  
 CC A method has been developed of initiating or enhancing: (i) an antigen-  
 CC specific immune tolerance; or (ii) immunotolerance of a therapeutic  
 CC immunogenic molecule by addition of a polypeptide, before, after or with  
 CC the mucosal administration of an immunotolerising amount of the antigen  
 CC or therapeutic molecule, respectively. The polypeptide is capable of  
 CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3  
 CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino  
 CC acids 28-y of human flt3-L, where y is an amino acid between 160-235;  
 CC and c) a polypeptide that has at least 90% identity to the polypeptides  
 CC of either (a) or (b). The method ameliorates the effects of autoimmune  
 CC diseases, food allergies or organ or tissue rejection following  
 CC transplantation. Administration of flt3-L allows lower doses of antigens  
 CC to be used in vivo for mucosally administered antigens. The present  
 CC sequence represents human flt3-L.  
 XX  
 SQ Sequence 235 AA;  
  
 Query Match 100.0%; Score 1242; DB 20; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-109;  
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60  
 DB 1 mtvalapawspptyllllllssgsgtqdcsfqhspsdsfavkirelsdyllqdyptv 60  
 QY 61 ASNQDEELCGGLRVLVLAQRWMERLKTVAAGSKKQGLLEVRNTEIHFTVTCARQPPPSCL 120  
 DB 61 asnlqdeelcggglrvlvaqrwmerlktvagskmgllervnteihvtkcatqpppscl 120  
 QY 121 RFVQTNISRLQETSEQLVAKPWITRONFSRCLELCCOPDSSFTLPPWSPRPLEATAPT 180  
 DB 121 rfvtgnisrllqetseqvlakpwitrgnfsrclelccqpdssclppwsprrpleatapt 180  
 QY 181 APQPLLILLLLPVGLLLAAAWCLHWQRTTRRRTPRGEQVPPVPSQDILLVEH 235  
 DB 181 apqpplllllllpvglilllaawclhwgrtrrrtrrpgeqvppvpqdillveh 235  
  
 RESULT 3  
 ID AAY69719 standard; Protein: 235 AA.  
 XX  
 AC AAY69719;  
 XX  
 DT 05-JUL-2000 (first entry)  
 XX  
 DE Full length wild type human flt-3 protein.  
 XX  
 KW Immunomodulator; immunosuppressive; cytostatic; anti-anemic; anti-HIV;  
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;  
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
 KW cellular expansion; cellular differentiation; natural killer cell;  
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
 KW multiple myeloma; leukemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200001823-A2.  
 PD 13-JAN-2000.



XX 25-JUN-1999: 99WO-US14296.  
XX 02-JUL-1998: 98US-0109100.  
XX (IMMUNEX CORP.  
XX Graddis TJ, McGrew JT;  
XX WPI: 2000-182115/16.  
XX N-PSDB: AA259064.  
XX  
XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,  
XX immune response stimulation or treatment of pathological conditions  
XX contains amino acid substitutions at positions 8, 84, 118 or 122 -  
XX  
XX Claim 1; Page 72-73; 90pp: English.  
XX  
XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides  
XX which exhibits increased or decreased biological activity relative to  
XX the full length wild type (this sequence) or mature (AA69720) flt3-L  
XX polypeptides. The flt3-L protein binds cell surface tyrosine kinase  
XX receptors and regulate growth and differentiation of hematopoietic  
XX progenitor cells. The flt3-L protein can be used to induce cellular  
XX expansion (especially in vivo) or differentiation, e.g. in  
XX hematopoietic, natural killer (NK) or dendritic cells, especially in the  
XX presence of growth factors such as interleukins, colony stimulating  
XX factors or protein kinases. The protein can also modulate, augment or  
XX enhance a patient's immune response and can be used to treat an immune  
XX disorder (e.g. allergy, autoimmunity or immunosuppression). The protein  
XX may be used to treat a pathological condition e.g. myelodysplasia,  
XX aplastic anemia, HIV infection, breast, small cell lung, testicular or  
XX ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute  
XX leukemia.  
XX  
XX Sequence 235 AA:  
SO  
Query Match 100.0%; Score 1242; DB 21; Length 235;  
Best Local Similarity 100.0%; Pred. No. 3.6e-109;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTVALPAMSPPTTYLLLLSSGSGTDCSFQHSPISSDFAVKIRELSDVLLADYPTV 60  
DB 1 mtvalapawspptyllllllssgsgtgdcsfqhspsidfavkirelsdyllqdyprtv 60  
QY 61 ASNLODELGGLMRLVLAQRWMERLKVAGSKMGGLERNTETHPYTKCAFQPPSCL 120  
DB 61 asnlqdeelcgglwrlvlagqrwmerlktvagskmggllerynteihvtkcafqppsc1 120  
QY 121 RFVQTNISRLQETSEQLVAKPMTTRQNFSCLELQCPDSSSTLPPMSPRPLEATAP 180  
DB 121 rfvtgnisrllqetseqlvalkpwtrnfnfsclelqcpdssclpppwsprpleatp 180  
QY 181 APQPELLELLPVGLLLLAAMCLHMQRTRRRPRPEQYVPVPSPODLLLVEN 235  
DB 181 apqpplllllllpygllllaaawclhmqrtrrrprpeqyvpvpspdllllven 235  
RESULT 4  
AAB20192  
ID AAB20192 standard; Protein: 235 AA.  
AC AAB20192;  
XX  
XX 14-MAY-2001 (first entry)  
XX  
XX Human Flt-3 ligand.  
XX  
XX Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;  
XX immunotherapy; therapy; tumour; cancer; melanoma; glioma;  
XX lymphoma; autoimmune disease; infection; gene therapy.  
XX

OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..26  
FT   
FT   
FT Protein /label= Signal\_peptide  
FT   
FT   
FT Domain /label= Mature\_protein  
FT   
FT Domain /label= Extracellular\_domain  
FT   
FT Domain /label= Transmembrane\_domain  
FT   
FT Domain /label= Cytoplasmic\_domain  
PN WO200109303-A2.  
PD 08-FEB-2001.  
XX  
XX 31-JUL-2000; 2000WO-US20679.  
XX  
XX 30-JUL-1999; 99US-0146170.  
XX  
XX (VICA-) VICAL INC.  
PA   
PI Hermanson GG;  
XX WPI: 2001-123319/13.  
XX N-PSDB: AAF30310.  
XX  
XX Immunogenic compositions comprising Flt-3 ligand encoding  
XX polynucleotide and one or more antigen, or cytokine encoding  
XX polynucleotides, useful for suppressing tumour growth and for treating  
XX autoimmune diseases (e.g. rheumatoid arthritis) -  
XX  
XX Claim 2; Page 132-133; 149pp: English.  
XX  
XX The present sequence is that of human Fms-like tyrosine kinase  
XX (Flt-3 ligand). The invention is directed to enhancing the  
XX immune response of a vertebrate to an antigen or a cytokine by  
XX administering in vivo, into a tissue of a vertebrate, a Flt-3  
XX ligand-encoding polynucleotide, and 1 or more antigen- or  
XX cytokine-encoding polynucleotides. The Flt-3 ligand-encoding  
XX polynucleotide may encode the present full-length human Flt-3  
XX ligand polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185,  
XX or 27-235 of the ligand. The polynucleotides are incorporated  
XX into the cells of the vertebrate in vivo, and a prophylactically  
XX or therapeutically effective amount of Flt-3 ligand and 1 or more  
XX antigens or cytokines is produced in vivo. Pharmaceutical  
XX compositions comprising the polynucleotides are useful for  
XX suppressing tumour growth in a mammal. The tumour is melanoma,  
XX glioma or lymphoma, particularly B-cell lymphoma. They can also  
XX be used for the prophylactic and/or therapeutic treatment of:  
XX (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B  
XX and C in humans), parasitic (e.g. malaria) and fungal infections;  
XX (b) autoimmune diseases (e.g. rheumatoid arthritis and  
XX osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.  
XX Various other examples of these diseases are given in the  
XX specification.  
XX  
XX Sequence 235 AA:  
SO  
Query Match 100.0%; Score 1242; DB 22; Length 235;  
Best Local Similarity 100.0%; Pred. No. 3.6e-109;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTVALPAMSPPTTYLLLLSSGSGTDCSFQHSPISSDFAVKIRELSDVLLADYPTV 60  
DB 1 mtvalapawspptyllllllssgsgtgdcsfqhspsidfavkirelsdyllqdyprtv 60  
QY 61 ASNLODELGGLMRLVLAQRWMERLKVAGSKMGGLERNTETHPYTKCAFQPPSCL 120  
DB 61 asnlqdeelcgglwrlvlagqrwmerlktvagskmggllerynteihvtkcafqppsc1 120

Oy	121	RFWONINISLLEOTSFQALAKPKWTRROWFSRCLFQQCPDSSSTLPPEMSPPLEATAPT	180
Oy	121	RVVQNNINSLLEOTSFQALAKPKWTRROWFSRCLFQQCPDSSSTLPPEMSPPLEATAPT	180
Db	121	rTvvqnninrlllqeteeaqvalkpwlrtqrfrfscleldgcpsdstllpppsprlpdeapt	180
Oy	181	AFOPPLLLLLLVPGILLAAAMCMLHMORTRRRTPRPGEQVPVPSPODLLVEH	235
Db	181	aqppllllllllvpgillllaaawclhwgrttrrrtpgsgvpyvpvpsqdlllvch	235
 RESULT 5			
ID	AAR6175	AAR6175 standard; Peptide: 235 AA.	
XX	AC	AAR6175;	
XX	DT	10-AUG-1995 (first entry)	
DE	XX	Human S86/S109 Flt3 ligand peptide sequence.	
KW	XX	Flt3 ligand; tyrosine kinase receptor ligand.	
OS	XX	Homo sapiens.	
PN	XX	WO9426891-A.	
PD	XX	24-NOV-1994.	
PF	XX	18-MAY-1994; 94WO-US05150.	
PR	XX	19-MAY-1993; 93US-0065231.	
PR	XX	07-JUL-1993; 93US-0089263.	
PR	XX	16-JUL-1993; 93US-0092549.	
PR	XX	13-AUG-1993; 93US-0106340.	
PR	XX	24-AUG-1993; 93US-0112391.	
PR	XX	19-NOV-1993; 93US-0155111.	
PR	XX	03-DEC-1993; 93US-0162413.	
PA	(INRM ) INST NAT SANTE & RECH MEDICALE.		
PA	(SCHE ) SCHERING CORP.		
PI	Birnbaum D, Culpepper JA, Hannum CH, Lee FD;		
DR	WP1: 1995-006787/01.		
XX	N-PSDB; AAO79642.		
PT	New ligand for the Flt3 tyrosine kinase receptor - and related		
PT	nucleic acid, vectors, host cells and antibodies, useful for		
PT	treatng abnormal cell physiology and proliferation, e.g. cancer,		
PT	also for diagnosis and drug screening		
PS	Claim 11; Page 76-77; 90pp; English.		
CC	XX	A CDNA library from the human stromal cell line 2S3V48, in	
CC	XX	pME18S, was screened with an 800 bp fragment derived from	
CC	XX	pME18S, clone T118. This fragment encompasses the coding region	
CC	XX	conserved between two mouse clones, T118 and T110. Approx. 20	
CC	XX	positive clones were selected and partially sequenced. Two	
CC	XX	clones, S86 and S109, were found to be approx. 75% homologous	
CC	XX	to the mouse clones over the first 163 AAs. Clone S86 continued	
CC	XX	to show homology to T110 until the stop codon, although to a	
CC	XX	lesser degree, for an overall homology of 66%. Clones T118 and	
CC	XX	S109 do not show homology to each other or to the other clones	
CC	XX	after mouse residue 163 (human residue 160). An additiona mouse	
CC	XX	clone designated M88 has a 29 AA insert at the junction between	
CC	XX	the common and divergent portions of the mouse ligand.	
SO	Sequence	235 AA:	
 ↓			
Query Match	99.5%;	Score 1236;	DB 16; Length 235;
Best Local Similarity	99.6%;	Pred. No. 1,3e+108;	
Matches 234%, Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;

Oy	1	MTVLAPAMSPPTVYLIIIIIISSGLSGTOPCSFQHPSPISSDFAVKIREDSDYLLADDPVTV	60
Oy	1	mtvlapamspptyllylllllssglsqtdcsiqnspissdfeavkiretsdyllqdyptv	60
Db	1	mtvlapamspptyllylllllssglsqtdcsiqnspissdfeavkiretsdyllqdyptv	60
Oy	61	ASNLDQDELGGIMRLVLAORMMERLKTAVAGSKMGLERVNTETIEFTVKAFQPPPSCL	120
Db	61	asnldqdelcgalmrlvlaqrmmelrktavagskmgllervntetieftvkafqpppscl	120
Oy	121	RFVQTNISRLQETSEQVLAIAKWTTRONFSCLELQCPDSSSTLPPEWSPPLEATAPT	180
Db	121	rftvqtnisrlqetseqvllaikpwtrqnfsclelqcpdssstlppwspplleatapt	180
Oy	181	APOPELLLLLLLPGLLLAAACCLIMORRRRTPPGQVPPVPSPODLLVEN	235
Db	181	apqppllllllllpvglllllaaacclimqrrrttrtpgqevppvpspdqlllven	235
RESULT	6		
AAB20194	ID	AAB20194 standard; Protein; 235 AA.	
XX	AC	AAB20194;	
XX	DT	14-MAY-2001 (first entry)	
XX	DE	Human Flt-3 ligand.	
XX	KW	Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;	
KW		immunotherapy; therapy; tumour; cancer; melanoma; glioma;	
KW		lymphoma; autoimmune disease; infection; gene therapy.	
XX	OS	Homo sapiens.	
XX	EH	Key	Location/Qualifiers
FT		Peptide	1..26
FT		Protein	/label= Signal_peptide
FT			27..235
FT		Domain	/label= Mature_protein
FT			27..182
FT		Domain	/label= Extracellular_domain
FT			183..205
FT		Domain	/label= Transmembrane_domain
FT			206..235
FT		Domain	/label= Cytoplasmic_domain
XX	PN	WO200109303-A2.	
XX	PD	08-FEB-2001.	
XX	PF	31-JUL-2000; 2000WO-US20679.	
XX	PR	30-JUL-1999; 99US-0146170.	
XX	RA	(VICAR-) VICAL INC.	
XX	PI	Hermanson GG;	
XX	DR	WPI: 2001-123319/13.	
XX	DR	N-PSDB; AAF30312.	
XX	PT	Immunogenic compositions comprising Flt-3 ligand encoding	
XX	PT	polynucleotide and one or more antigen, or cytokine encoding	
XX	PT	polynucleotides, useful for suppressing tumour growth and for	
XX	PT	autoimmune diseases (e.g. rheumatoid arthritis) -	
XX	PS	Claim 2; Page 137-138; 149pp; English.	
CC		The present sequence is that of human Fms-like tyrosine kinase	
CC		(Flt-3 ligand). The invention is directed to enhancing the	
CC		immune response of a vertebrate to an antigen or a cytokine by	
CC		administering in vivo, into a tissue of a vertebrate, a Flt-3	
CC		ligand-encoding polynucleotide, and 1 or more antigen- or	

CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding  
CC polynucleotide may encode the present full-length human Flt-3  
CC ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235  
CC of the Flt-3 ligand. The polynucleotides are incorporated into  
CC the cells of the vertebrate in vivo, and a prophylactically or  
CC therapeutically effective amount of Flt-3 ligand and 1 or more  
CC antigens or cytokines is produced in vivo. Pharmaceutical  
CC compositions comprising the polynucleotides are useful for  
CC suppressing tumour growth in a mammal. The tumour is melanoma,  
CC glioma or lymphoma, particularly B-cell lymphoma. They can also  
CC be used for the prophylactic and/or therapeutic treatment of:  
CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B  
CC and C in humans), parasitic (e.g. malaria) and fungal infections;  
CC (b) autoimmune diseases (e.g. rheumatoid arthritis and  
CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.  
CC Various other examples of these diseases are given in the  
CC specification.  
CC  
CC  
SQ Sequence 235 AA:  
  
Query Match 99.5%; Score 1236; DB 22; Length 235;  
Best Local Similarity 99.6%; Pred. No. 1.3e-108;  
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
OY 1 MTVALPAPMSPTTYLLLLSSGLSGTQDSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60  
DB 1 mtlvalpawspptyllllllssglsqgdcsgfshpslssdfavkirelsdylldqypvtv 60  
  
OY 61 ASNLODELCGLMRLVLAQRMERLKTAVAGSKMGLLELVNTEHFVTKCAFQPPPSCL 120  
DB 61 asnlodeelcglmrlvlraqrmerlktvagskmgllervntehtfkcafqppsccl 120  
  
OY 121 RFVQNTISRLLQETSEQLVAKPWITRQNFRCLELQCPBSSFTLPWPWSRPLEATAPT 180  
DB 121 rfvqntisrllqetseqlvalkpwitrqnfrclelqcpbssftlpwpwsrpleatapt 180  
  
OY 181 APQPLLLLLLPYGLLLAAAMCLHMQRTRRRTPRCEQVPVPSPODLLVEH 235  
DB 181 apqplllllllpygllllaaamclhmqrtrrrtrrprgeqvpvpspdqlllveh 235  
  
RESULT 7  
AAV69721 ID AAV69721 standard; Protein; 212 AA.  
XX  
AC AAV69721;  
XX  
DT 05-JUL-2000 (first entry)  
XX  
DE Human flt-3 mutein L-3H.  
XX  
KW Immunomodulator; immunosuppressive; cytostatic; antineoplastic; anti-HIV;  
KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;  
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
KW cellular expansion; cellular differentiation; natural killer cell;  
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
KW multiple myeloma; leukemia; mutein.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
PN WO200001823-A2.  
XX  
PD 13-JAN-2000.  
XX  
XX 25-JUN-1999; 99WO-US14296.  
PF  
XX 02-JUL-1998; 98US-0109100.  
PR  
XX (IMMUNEX ) IMMUNEX CORP.  
PA  
XX

PI Gradis TJ, McGrew JT;  
XX  
DR WPI: 2000-182115/16.  
XX  
PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,  
PT immune response stimulation or treatment of pathological conditions  
PT contains amino acid substitutions at positions 8, 84, 118 or 122 -  
XX  
PS Claim 4; Page 79-80; 90pp; English.  
XX  
XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides  
CC which exhibits increased or decreased biological activity relative to  
CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L.  
CC polypeptides. This sequence represents an example of the novel flt-3  
CC ligands and comprises the L-3H mutant polypeptide. The flt3-L protein  
CC binds cell surface tyrosine kinase receptors and regulate growth and  
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can  
CC be used to induce cellular expansion (especially in vivo) or  
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic  
CC cells, especially in the presence of growth factors such as interleukins,  
CC colony stimulating factors or protein kinases. The protein can also  
CC modulate, augment or enhance a patient's immune response and can be used  
CC to treat an immune disorder (e.g. allergy, autoimmunity or  
CC immunosuppression). The protein may be used to treat a pathological  
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,  
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple  
CC myeloma, neuroblastoma or acute leukemia.  
XX  
SQ Sequence 212 AA:  
  
Query Match 90.5%; Score 1124; DB 21; Length 212;  
Best Local Similarity 100.0%; Pred. No. 4.2e-98;  
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 25 SGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVVASNLQDELCGLMRLVLAQRME 84  
DB 2 sgtqdcsgfshpslssdfavkirelsdylldqypvvasnldelcglmrlvlraqrme 84  
  
OY 85 RLKTYAGSKMGLLELVNTEHFVTKCAFQPPPSCLRFVQNTISRLLQETSEQLVAKPW 144  
DB 85 rlktyagskmgllervntehtfkcafqpppsclrfvqntisrllqetseqlvalkpw 144  
  
OY 62 RLKTYAGSKMGLLELVNTEHFVTKCAFQPPPSCLRFVQNTISRLLQETSEQLVAKPW 121  
DB 62 rlktyagskmgllervntehtfkcafqpppsclrfvqntisrllqetseqlvalkpw 121  
  
OY 145 ITRQNFRCLELQCPBSSFTLPWPWSRPLEATAPTAPQPLLLLLPYGLLLAAAMC 204  
DB 145 itrqnfrclelqcpbssftlpwpwsrpleataptapqplllllllpygllllaaamc 204  
  
OY 122 ITRQNFRCLELQCPBSSFTLPWPWSRPLEATAPTAPQPLLLLLPYGLLLAAAMC 181  
DB 122 itrqnfrclelqcpbssftlpwpwsrpleataptapqplllllllpygllllaaamc 181  
  
OY 205 LHMQRTRRRTPRCEQVPVPSPODLLVEH 235  
DB 205 lhmqrtrrrtrrprgeqvpvpspdqlllveh 235  
  
RESULT 8  
AAW69007 ID AAW69007 standard; Peptide; 209 AA.  
XX  
AC AAW69007;  
XX  
DT 01-OCT-1998 (first entry)  
XX  
DE Human flt-3 receptor agonist.  
XX  
KW Human; flt-3 receptor agonist; hematopoietic cell stimulation; cancer;  
KW bone marrow reconstruction; haematological disease; immune deficiency;  
KW drug-induced myelosuppression; renal dialysis; gene therapy; infection;  
KW congenital metabolic disease; neurological disease; therapy;  
KW dendritic cell production.  
XX  
XX Homo sapiens.  
OS  
XX W09818923-A1.  
PN  
XX 07-MAY-1998.  
PD



AAV69723 14  
ID AAV69723 standard; Protein: 209 AA.  
XX  
AC AAV69723;  
DT 05-JUL-2000 (first entry)  
XX  
DE Human flt-3 mutein K84E.  
XX  
KW Immunomodulator; immunosuppressive; cytostatic; antitumor; anti-HIV;  
KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;  
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
KW cellular expansion; cellular differentiation; natural killer cell;  
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
KW multiple myeloma; leukemia; mutein.  
XX  
OS Homo sapiens.  
OS Synthetic.  
PN WO200001823-A2.  
PD 13-JAN-2000.  
XX  
XX 25-JUN-1999; 99WO-US14296.  
PF 02-JUL-1998; 98US-0109100.  
PR  
XX (IMMV ) IMMUNEX CORP.  
XX  
PI Graddis TJ, McGrew JT;  
XX  
DR WPI: 2000-182115/16.  
XX  
PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,  
XX immune response stimulation or treatment of pathological conditions  
XX contains amino acid substitutions at positions 8, 84, 118 or 122 -  
XX  
PS Claim 4; Page 84-85; 90pp; English.  
XX  
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides  
CC which exhibits increased or decreased biological activity relative to  
CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L  
CC polypeptides. This sequence represents an example of the novel flt-3  
CC ligands and comprises the K84E mutant polypeptide. The flt3-L protein  
CC binds cell surface tyrosine kinase receptors and regulate growth and  
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can  
CC be used to induce cellular expansion (especially in vivo) or  
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic  
CC cells, especially in the presence of growth factors such as interleukins,  
CC colony stimulating factors or protein kinases. The protein can also  
CC modulate, augment or enhance a patient's immune response and can be used  
CC to treat an immune disorder (e.g. allergy, autoimmunity or  
CC immunosuppression). The protein may be used to treat a pathological  
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,  
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple  
CC myeloma, neuroblastoma or acute leukemia.  
XX  
XX Sequence 209 AA;  
SQ

Query Match 89.4%; Score 1110; DB 21; Length 209;  
Best Local Similarity 99.5%; Pred. No. 8.5e-97;  
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TQDSFGHSPISSDPFAVKIRELSLDYLDQVYVNASNLQDEELGGLRWLVLAQRMMERL 86  
DB 1 tqdcsfgspissd f a v k i r e l s d y l d q v y v n a s n l q d e e l g g l r w l v l a q r m m e r l 60  
QY 87 KTVASGKMOGLIERVNTIEHFVTKARQPPSCLEFVQNTISRLQOESEQLVAKPWT 146  
DB 61 k t v a s g k m o g l i e r v n t i e h f v t k a r q p p s c l e f v q n t i s r l q o e s e q l v a k p w t 120

QY 147 RQNFSCLELQCCPDSSSTLPPPMSPRLPEATAPTAPOPDLLLLLPVGLLLAAAMCLH 206  
DB 121 r q n f s c l e l q c c p d s s s t l p p p m s p r l p e a t a p t a p o p d l l l l p v g l l l a a a m c l h 180  
QY 207 WQTRRRRTPRPGEQVPPVPSQDLLLVEH 235  
DB 181 w q t r r r r t p r p g e q v p p v p s p q d l l l v e h 209

RESULT 11  
AAV69726  
ID AAV69726 standard; Protein: 209 AA.  
XX  
AC AAV69726;  
DT 05-JUL-2000 (first entry)  
XX  
DE Human flt-3 mutein Q122R.  
XX  
KW Immunomodulator; immunosuppressive; cytostatic; antitumor; anti-HIV;  
KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;  
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
KW cellular expansion; cellular differentiation; natural killer cell;  
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
KW multiple myeloma; leukemia; mutein.  
XX  
OS Homo sapiens.  
OS Synthetic.  
PN WO200001823-A2.  
PD 13-JAN-2000.  
XX  
XX 25-JUN-1999; 99WO-US14296.  
PF 02-JUL-1998; 98US-0109100.  
PR  
XX (IMMV ) IMMUNEX CORP.  
XX  
PI Graddis TJ, McGrew JT;  
XX  
DR WPI: 2000-182115/16.  
XX  
PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,  
XX immune response stimulation or treatment of pathological conditions  
XX contains amino acid substitutions at positions 8, 84, 118 or 122 -  
XX  
PS Claim 4; Page 88-89; 90pp; English.  
XX  
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides  
CC which exhibits increased or decreased biological activity relative to  
CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L  
CC polypeptides. This sequence represents an example of the novel flt-3  
CC ligands and comprises the Q122R mutant polypeptide. The flt3-L protein  
CC binds cell surface tyrosine kinase receptors and regulate growth and  
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can  
CC be used to induce cellular expansion (especially in vivo) or  
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic  
CC cells, especially in the presence of growth factors such as interleukins,  
CC colony stimulating factors or protein kinases. The protein can also  
CC modulate, augment or enhance a patient's immune response and can be used  
CC to treat an immune disorder (e.g. allergy, autoimmunity or  
CC immunosuppression). The protein may be used to treat a pathological  
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,  
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple  
CC myeloma, neuroblastoma or acute leukemia.  
XX  
XX Sequence 209 AA;  
SQ

Query Match 89.4%; Score 1110; DB 21; Length 209;  
Best Local Similarity 99.5%; Pred. No. 8.5e-97;









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OM protein - protein search, using sw model

Run on: April 1, 2002, 06:13:54 ; Search time 64.79 Seconds  
(without alignments)  
81.622 Million cell updates/sec

Title: US-08-162-407-6

Perfect score: 1242

Sequence: 1 MVLAPAMSPPTLYLLLLLL.....RPEQVPVPSPDLLVEH 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCrUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	235	1 US-08-243-545-6	Sequence 6, Appl1
2	1242	100.0	235	2 US-08-993-962-6	Sequence 6, Appl1
3	1242	100.0	235	4 US-09-160-841-6	Sequence 6, Appl1
4	1242	100.0	235	4 US-09-109-100-1	Sequence 6, Appl1
5	1242	100.0	235	5 PCT-US94-05365-6	Sequence 6, Appl1
6	1124	90.5	212	4 US-09-109-100-10	Sequence 10, Appl1
7	1114	89.7	209	4 US-09-109-100-18	Sequence 10, Appl1
8	1110	89.4	209	4 US-09-109-100-9	Sequence 18, Appl1
9	1110	89.4	209	4 US-09-109-100-12	Sequence 9, Appl1
10	1110	89.4	209	4 US-09-109-100-14	Sequence 12, Appl1
11	1110	89.4	209	4 US-09-109-100-11	Sequence 14, Appl1
12	1108	89.2	209	4 US-09-109-100-15	Sequence 17, Appl1
13	1108	89.2	209	4 US-09-109-100-15	Sequence 11, Appl1
14	1107	89.1	209	4 US-09-109-100-13	Sequence 15, Appl1
15	1106	89.0	209	4 US-09-109-100-8	Sequence 13, Appl1
16	1100	88.6	209	4 US-09-109-100-16	Sequence 8, Appl1
17	768.5	61.9	231	1 US-08-243-545-2	Sequence 16, Appl1
18	768.5	61.9	231	2 US-08-993-962-2	Sequence 2, Appl1
19	768.5	61.9	231	2 US-09-160-841-2	Sequence 2, Appl1
20	768.5	61.9	231	5 PCT-US94-05365-2	Sequence 2, Appl1
21	765.5	61.6	231	1 US-08-220-319B-7	Sequence 2, Appl1
22	765.5	61.6	231	5 PCT-US95-03866-6	Sequence 7, Appl1
23	506.5	40.8	137	4 US-09-109-100-19	Sequence 6, Appl1
24	154	12.4	42	5 PCT-US94-05150-17	Sequence 19, Appl1
25	91.5	7.4	675	1 US-08-317-522A-9	Sequence 17, Appl1
26	91.5	7.4	675	1 US-08-439-818A-9	Sequence 9, Appl1
27	91.5	7.4	675	2 US-08-751-965-9	Sequence 9, Appl1

28	91.5	7.4	675	2 US-08-738-975-9	Sequence 9, Appl1
29	91.5	7.4	675	2 US-08-728-626-9	Sequence 9, Appl1
30	91.5	7.4	675	3 US-08-808-599A-9	Sequence 9, Appl1
31	87.5	7.0	415	4 US-09-006-353A-6	Sequence 6, Appl1
32	85	6.8	366	1 US-08-004-492-8	Sequence 8, Appl1
33	84.5	6.8	913	3 US-08-445-640-4	Sequence 4, Appl1
34	84.5	6.8	913	3 US-08-170-558-4	Sequence 4, Appl1
35	84.5	6.8	913	3 US-08-447-314-4	Sequence 4, Appl1
36	84.5	6.8	913	3 US-08-445-461-4	Sequence 4, Appl1
37	84	6.8	107	4 US-09-220-528-52	Sequence 52, Appl1
38	84	6.8	220	4 US-09-220-528-26	Sequence 26, Appl1
39	83.5	6.7	429	1 US-07-964-589-2	Sequence 2, Appl1
40	83.5	6.7	429	5 PCT-US93-02024-2	Sequence 2, Appl1
41	83.5	6.7	671	3 US-09-121-321-16	Sequence 16, Appl1
42	83.5	6.7	671	4 US-08-933-803A-16	Sequence 16, Appl1
43	83	6.7	28	5 PCT-US94-05150-12	Sequence 12, Appl1
44	83	6.7	758	1 US-07-756-250-16	Sequence 16, Appl1
45	82.5	6.6	249	2 US-08-632-514C-11	Sequence 11, Appl1

## ALIGNMENTS

RESULT 1  
US-08-243-545-6  
: Sequence 6, Application US/08243545  
: Patent No. 5554512  
: GENERAL INFORMATION:  
: APPLICANT: Lyman, Stewart D.  
: APPLICANT: Beckmann, M. Patricia  
: TITLE OF INVENTION: Ligands for f1c3/flk-2 Receptors  
: NUMBER OF SEQUENCES: 8  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Stephen U. Malaska, Immunex Corporation  
: STREET: 51 University Street  
: CITY: Seattle  
: STATE: Washington  
: COUNTRY: US  
: ZIP: 98101  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: OPERATING SYSTEM: Macintosh 7.0.1  
: SOFTWARE: Microsoft Word, Version #5.1  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/243,545  
: FILING DATE: 11-MAY-1994  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/162,407  
: FILING DATE: 03-DEC-1993  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 08/111,758  
: FILING DATE: August 25, 1993  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 08/106,463  
: FILING DATE: August 12, 1993  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 08/068,394  
: FILING DATE: May 24, 1993  
: CLASSIFICATION: 435  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Malaska, Stephen U.  
: REGISTRATION NUMBER: 32,655  
: REFERENCE/DOCKET NUMBER: 2813-C  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (206) 587-0430  
: TELEFAX: (206) 233-0644  
: TELETYPE: 755622  
: INFORMATION FOR SEQ ID NO: 6:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 235 amino acids

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;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-243-545-6

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Query Match	100.0%;	Score 1242;	DB 1;	Length 235;
Best Local Similarity	100.0%;	Pred. No. 1.4e-117;		
Matches 235; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Qy	1	MTVLAPAMSPPTTYLLLLLLSSGSLGQDSCFOHSPISSPFANVIRLSLYLLQDYYVW	60
Db	1	MTVLAPAMSPPTTYLLLLLLSSGSLGQDSCFOHSPISSPFANVIRLSLYLLQDYYVW	60
Qy	61	ASNLQDEBLCGGLRWLYLAQRMERLKTVAAGSKMOGLIERNTEIHHVYTKCAFQPPSCL	120
Db	61	ASNLQDEBLCGGLRWLYLAQRMERLKTVAAGSKMOGLIERNTEIHHVYTKCAFQPPSCL	120
Qy	121	RFVQTNISRLLQETSEQVALKPKPITTKQNSRCLCLOCQDPSSTLPPWGSRLPLEATAPT	180
Db	121	RFVQTNISRLLQETSEQVALKPKPITTKQNSRCLCLOCQDPSSTLPPWGSRLPLEATAPT	180
Qy	181	APQPPLLLLLLLPVGLLLAAAMCLHMQTRRRTPRQGEQVPPVPSQDILLVEH	235
Db	181	APQPPLLLLLLLPVGLLLAAAMCLHMQTRRRTPRQGEQVPPVPSQDILLVEH	235

RESULT 2  
US-08-993-962-6  
; Sequence 6, Application US/08993962

GENERAL INFORMATION:  
APPLICANT: Lyman, Stewart D.  
APPLICANT: Beckmann, M. Patricia  
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
219, 08101

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1: COMPUTER READABLE FORM:
2: MEDIUM TYPE: Floppy disk
3: COMPUTER: Apple Macintosh
4: OPERATING SYSTEM: Macintosh 7.0.1
5: SOFTWARE: Microsoft Word, Version #5.1
6: CURRENT APPLICATION DATA:
7: APPLICATION NUMBER: US/08/993,962
8: FILING DATE: December 18, 1997

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TELEX: 756622  
INFORMATION FOR SEQ ID NO: 6  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-993-962-6

Query Match	100.0%;	Score 1242;	DB 2;	Length 235;
Best Local Similarity	100.0%;	Pred. No. 1.4e-117;		
Matches 235; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	MTVAPAMSPPTTYLLELLLELLSSGSGSGQDSCFQHSPISSPFAKIRELSYLLQDYPVY	60
Db	1	MTVAPAMSPPTTYLLELLLELLSSGSGSGQDSCFQHSPISSPFAKIRELSYLLQDYPVY	60
QY	61	ASNLQDEELCGGLMWRLVLAQRMWERLKTVAAGSKMQGILLERVNTEIHFWTKCAFQPPSCL	120
Db	61	ASNLQDEELCGGLMWRLVLAQRMWERLKTVAAGSKMQGILLERVNTEIHFWTKCAFQPPSCL	120
QY	121	RFVQTNISRLLQETSEBDVALKPRITRQNSRCLCLOCPDSSTLPPWSPRLLEATAP	180
Db	121	RFVQTNISRLLQETSEBDVALKPRITRQNSRCLCLOCPDSSTLPPWSPRLLEATAP	180
QY	181	APQPPILLLELLPGVLLLLAAMCLHMQRTRRRPRRGEQVPVPSQDILLVEH	235
Db	181	APQPPILLLELLPGVLLLLAAMCLHMQRTRRRPRRGEQVPVPSQDILLVEH	235

RESULT 3  
US-09-160-841-6  
: Sequence 6, Application US/09160841

GENERAL INFORMATION:  
APPLICANT: Lyman, Stewart D.  
APPLICANT: Beckmann, M Patricia  
TITLE OF INVENTION: Ligands for flk-2 Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101

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? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: Apple Macintosh
? OPERATING SYSTEM: Macintosh 7.0.1
? SOFTWARE: Microsoft Word, Version #5.1.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: 05/09/160,841

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;; CURRENT FILING DATE: 1998-07-02  
;; NUMBER OF SEQ ID NOS: 20  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 12  
;; LENGTH: 209  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-109-100-12

Query Match 89.4%; Score 1110; DB 4; Length 209;  
Best Local Similarity 99.5%; Pred. No. 2.4e-104;  
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 27 TODCSFQHSPISSDFAVKIRELSYLLDYPYTVASNLQDEELCGMLRVLAORMERL 86  
DB 1 TODCSFQHSPISSDFAVKIRELSYLLDYPYTVASNLQDEELCGMLRVLAORMERL 60  
OY 87 KTVAGSKMOGLLEERVNTEIHFTKCAFOPPPSCLRFVQTNISRLQETSEQVALKPWIT 146  
DB 61 KTVAGSKMOGLLEERVNTEIHFTKCAFOPPPSCLRFVQTNISRLQETSEQVALKPWIT 120  
OY 147 RQNFSCRLELQOCQPDSSSTLPPWSPRPLEATAPAPQPLLLLLPVGLLLAAACMLH 206  
DB 121 RQNFSCRLELQOCQPDSSSTLPPWSPRPLEATAPAPQPLLLLLPVGLLLAAACMLH 180  
OY 207 WQTRRRTPRPEQVPPVPSPODLLVEH 235  
DB 181 WQTRRRTPRPEQVPPVPSPODLLVEH 209

RESULT 10  
US-09-109-100-14  
;; Sequence 14, Application US/09109100C  
;; Patent No. 6291661  
;; GENERAL INFORMATION:  
;; APPLICANT: Graddis, Thomas J.  
;; APPLICANT: McGrew, Jeffrey T.  
;; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
;; FILE REFERENCE: 03260.0028  
;; CURRENT APPLICATION NUMBER: US/09/109,100C  
;; CURRENT FILING DATE: 1998-07-02  
;; NUMBER OF SEQ ID NOS: 20  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 14  
;; LENGTH: 209  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-109-100-14

Query Match 89.4%; Score 1110; DB 4; Length 209;  
Best Local Similarity 99.5%; Pred. No. 2.4e-104;  
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 27 TODCSFQHSPISSDFAVKIRELSYLLDYPYTVASNLQDEELCGMLRVLAORMERL 86  
DB 1 TODCSFQHSPISSDFAVKIRELSYLLDYPYTVASNLQDEELCGMLRVLAORMERL 60  
OY 87 KTVAGSKMOGLLEERVNTEIHFTKCAFOPPPSCLRFVQTNISRLQETSEQVALKPWIT 146  
DB 61 KTVAGSKMOGLLEERVNTEIHFTKCAFOPPPSCLRFVQTNISRLQETSEQVALKPWIT 120  
OY 147 RQNFSCRLELQOCQPDSSSTLPPWSPRPLEATAPAPQPLLLLLPVGLLLAAACMLH 206  
DB 121 RQNFSCRLELQOCQPDSSSTLPPWSPRPLEATAPAPQPLLLLLPVGLLLAAACMLH 180  
OY 207 WQTRRRTPRPEQVPPVPSPODLLVEH 235  
DB 181 WQTRRRTPRPEQVPPVPSPODLLVEH 209

RESULT 11

US-09-109-100-17  
;; Sequence 17, Application US/09109100C  
;; Patent No. 6291661  
;; GENERAL INFORMATION:  
;; APPLICANT: Graddis, Thomas J.  
;; APPLICANT: McGrew, Jeffrey T.  
;; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
;; FILE REFERENCE: 03260.0028  
;; CURRENT APPLICATION NUMBER: US/09/109,100C  
;; CURRENT FILING DATE: 1998-07-02  
;; NUMBER OF SEQ ID NOS: 20  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 17  
;; LENGTH: 209  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-109-100-17

Query Match 89.4%; Score 1110; DB 4; Length 209;  
Best Local Similarity 99.5%; Pred. No. 2.4e-104;  
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 27 TODCSFQHSPISSDFAVKIRELSYLLDYPYTVASNLQDEELCGMLRVLAORMERL 86  
DB 1 TODCSFQHSPISSDFAVKIRELSYLLDYPYTVASNLQDEELCGMLRVLAORMERL 60  
OY 87 KTVAGSKMOGLLEERVNTEIHFTKCAFOPPPSCLRFVQTNISRLQETSEQVALKPWIT 146  
DB 61 KTVAGSKMOGLLEERVNTEIHFTKCAFOPPPSCLRFVQTNISRLQETSEQVALKPWIT 120  
OY 147 RQNFSCRLELQOCQPDSSSTLPPWSPRPLEATAPAPQPLLLLLPVGLLLAAACMLH 206  
DB 121 RQNFSCRLELQOCQPDSSSTLPPWSPRPLEATAPAPQPLLLLLPVGLLLAAACMLH 180  
OY 207 WQTRRRTPRPEQVPPVPSPODLLVEH 235  
DB 181 WQTRRRTPRPEQVPPVPSPODLLVEH 209

RESULT 12  
US-09-109-100-11  
;; Sequence 11, Application US/09109100C  
;; Patent No. 6291661  
;; GENERAL INFORMATION:  
;; APPLICANT: Graddis, Thomas J.  
;; APPLICANT: McGrew, Jeffrey T.  
;; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
;; FILE REFERENCE: 03260.0028  
;; CURRENT APPLICATION NUMBER: US/09/109,100C  
;; CURRENT FILING DATE: 1998-07-02  
;; NUMBER OF SEQ ID NOS: 20  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 11  
;; LENGTH: 209  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-109-100-11

Query Match 89.2%; Score 1108; DB 4; Length 209;  
Best Local Similarity 99.5%; Pred. No. 3.8e-104;  
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 27 TODCSFQHSPISSDFAVKIRELSYLLDYPYTVASNLQDEELCGMLRVLAORMERL 86  
DB 1 TODCSFQHSPISSDFAVKIRELSYLLDYPYTVASNLQDEELCGMLRVLAORMERL 60  
OY 87 KTVAGSKMOGLLEERVNTEIHFTKCAFOPPPSCLRFVQTNISRLQETSEQVALKPWIT 146  
DB 61 KTVAGSKMOGLLEERVNTEIHFTKCAFOPPPSCLRFVQTNISRLQETSEQVALKPWIT 120  
OY 147 RQNFSCRLELQOCQPDSSSTLPPWSPRPLEATAPAPQPLLLLLPVGLLLAAACMLH 206

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Db 121 RONSRCLELQCCOPDSSSTLPPMSPRPLEATAPAPQPLLLLLLLPVGLLLAAACLH 180
OY 207 WQTRRRTPRPGEOVPPVPSPODLLVEH 235
Db 181 WQTRRRTPRPGEOVPPVPSPODLLVEH 209

RESULT 13
US-09-109-100-15
; Sequence 15, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: McGraddis, Thomas J.
; APPLICANT: McGraddis, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; LENGTH: 209
; SEQ ID NO 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-15

Query Match 89.2%; Score 1108; DB 4; Length 209;
Best local Similarity 99.5%; Pred. No. 3.8e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLMRLVLAQRMMERL 86
Db 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLMRLVLAQRMMERL 60

OY 87 KTVAGSKMOGLLEVRNTEIHVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPMIT 146
Db 61 KTVAGSKMOGLLEVRNTEIHVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPMIT 120

OY 147 RONSRCLELQCCOPDSSSTLPPMSPRPLEATAPAPQPLLLLLLLPVGLLLAAACLH 206
Db 121 RONSRCLELQCCOPDSSSTLPPMSPRPLEATAPAPQPLLLLLLLPVGLLLAAACLH 180

OY 207 WQTRRRTPRPGEOVPPVPSPODLLVEH 235
Db 181 WQTRRRTPRPGEOVPPVPSPODLLVEH 209

RESULT 14
US-09-109-100-13
; Sequence 13, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: McGraddis, Thomas J.
; APPLICANT: McGraddis, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-13

Query Match 89.1%; Score 1107; DB 4; Length 209;
Best local Similarity 99.5%; Pred. No. 4.8e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLMRLVLAQRMMERL 86
Db 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLMRLVLAQRMMERL 60

OY 87 KTVAGSKMOGLLEVRNTEIHVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPMIT 146
Db 61 KTVAGSKMOGLLEVRNTEIHVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPMIT 120

OY 147 RONSRCLELQCCOPDSSSTLPPMSPRPLEATAPAPQPLLLLLLLPVGLLLAAACLH 206
Db 121 RONSRCLELQCCOPDSSSTLPPMSPRPLEATAPAPQPLLLLLLLPVGLLLAAACLH 180

OY 207 WQTRRRTPRPGEOVPPVPSPODLLVEH 235
Db 181 WQTRRRTPRPGEOVPPVPSPODLLVEH 209

RESULT 15
US-09-109-100-8
; Sequence 8, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: McGraddis, Thomas J.
; APPLICANT: McGraddis, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-8

Query Match 89.0%; Score 1106; DB 4; Length 209;
Best local Similarity 99.5%; Pred. No. 6.1e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLMRLVLAQRMMERL 86
Db 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLMRLVLAQRMMERL 60

OY 87 KTVAGSKMOGLLEVRNTEIHVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPMIT 146
Db 61 KTVAGSKMOGLLEVRNTEIHVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPMIT 120

OY 147 RONSRCLELQCCOPDSSSTLPPMSPRPLEATAPAPQPLLLLLLLPVGLLLAAACLH 206
Db 121 RONSRCLELQCCOPDSSSTLPPMSPRPLEATAPAPQPLLLLLLLPVGLLLAAACLH 180

OY 207 WQTRRRTPRPGEOVPPVPSPODLLVEH 235
Db 181 WQTRRRTPRPGEOVPPVPSPODLLVEH 209
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Search completed: April 1, 2002, 06:16:38  
Job time: 164 sec

Mon Apr 1 06:15:15 2002

us-08-162-407-6.rai

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Page 7

